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OM protein - protein search, using sw model

Run on: July 18, 2002, 10:12:53 ; Search time 29.96 Seconds  
(without alignments)  
37.074 Million cell updates/sec

Title: US-09-724-842-27

Perfect score: 55

Sequence: 1 HHQKLVFFAQ 10

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A: Geneseq 032802.\*  
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
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19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	22	AA82641 All-D peptide used
2	55	100.0	28	17	AAW01414 Beta/A4-amyloid pe
3	55	100.0	28	22	AA835600 Human clone E220 B
4	55	100.0	35	22	AA891803 Amyloid beta-prote
5	55	100.0	35	22	AA891830 Amyloid beta-prote
6	55	100.0	40	19	AAW47232 Beta-amyloid pepti
7	55	100.0	53	15	AAW55697 Sequence of uniden
8	55	100.0	63	18	AAW26511 Amyloid precursor
9	55	100.0	63	18	AAW26391 Amyloid precursor
10	55	100.0	63	19	AAW44746 APP-RFP 751 [BAP E
11	55	100.0	63	19	AAW42975 Beta-amyloid pepti

12	55	100.0	99	16	AA874595 Beta-amyloid precu
13	52	94.5	10	22	AA846225 Human APP derived
14	52	94.5	15	20	AAW89358 Beta-amyloid pepti
15	52	94.5	17	15	AA854703 Beta-amyloid fragm
16	52	94.5	17	22	AA891774 Amyloid beta-prote
17	52	94.5	17	22	AA891807 Amyloid beta-prote
18	52	94.5	17	22	AA848346 Beta-amyloid anti
19	52	94.5	18	21	AA810963 Beta-amyloid precu
20	52	94.5	19	18	AAW18882 AEDANS-beta-amyloi
21	52	94.5	19	18	AAW18881 Trip-Beta-amyloid p
22	52	94.5	19	22	AA846201 Human APP A-beta 1
23	52	94.5	19	22	AA849097 Human amyloid beta
24	52	94.5	21	20	AA830941 Human secretase SE
25	52	94.5	24	15	AA852569 Alzheimer's diseas
26	52	94.5	26	19	AAW47229 Beta-amyloid pepti
27	52	94.5	26	20	AA833408 Human amyloidogeni
28	52	94.5	27	20	AA833409 Human amyloidogeni
29	52	94.5	28	8	AA870594 Sequence of Alzhei
30	52	94.5	28	10	AA890381 Synthetic A4 amylo
31	52	94.5	28	15	AA854702 Beta-amyloid fragm
32	52	94.5	28	15	AA860368 Beta-amyloid (1-28
33	52	94.5	28	16	AA864170 A4-O(1-28) a parti
34	52	94.5	28	16	AA864171 A4-P(1-28) a parti
35	52	94.5	28	16	AA864172 A4-B(1-28) a parti
36	52	94.5	28	16	AA864164 Generic beta amylo
37	52	94.5	28	17	AAW01413 Beta/A4-amyloid pe
38	52	94.5	28	20	AA839805 Synthetic amyloid
39	52	94.5	28	20	AAW81467 Amyloid beta-prote
40	52	94.5	28	22	AA891783 Amyloid beta-prote
41	52	94.5	28	22	AA891789 Amyloid beta-prote
42	52	94.5	28	22	AA891800 Amyloid beta-prote
43	52	94.5	28	22	AA891816 Amyloid beta-prote
44	52	94.5	28	22	AA891827 Amyloid beta-prote
45	52	94.5	28	22	AA849396 Human amyloid pept

#### ALIGNMENTS

RESULT 1  
AA82641  
ID AA82641 standard; Peptide; 10 AA.  
XX  
AC AA82641;  
XX  
DT 02-OCT-2001 (first entry)  
XX  
DE All-D peptide used in Alzheimer's disease vaccine.  
XX  
KW Alzheimer's disease; amyloidosis; amyloid-related disease;  
XX vaccine; therapy; antigen.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..10 /note= "all D-form residues"  
FT  
XX  
PN WO200139796-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 29-NOV-2000; 2000WO-CA01413.  
XX  
PR 29-NOV-1999; 99US-0168594.  
XX  
PR 28-NOV-2000; 2000US-0724842.  
XX  
PA (NEUR-) NEUROCHEM INC.  
XX  
PI Chalifour R, Hebert L, Kong X, Gervais F;  
XX WPI; 2001-441458/47.  
XX

PT Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, e.g. as  
 PT vaccine, which elicits production of antibodies to prevent  
 PT fibrillogenesis and associated cellular toxicity -

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for  
 CC use in preparing vaccines for preventing or treating Alzheimer's  
 CC disease and other amyloid related disorders in humans. It is based  
 CC on a portion of amyloid-beta peptide (see AAB82622) and may be  
 CC modified by removing or inserting 1 or more amino acid residues, or  
 CC by substituting 1 or more amino acid residues with other amino acid  
 CC residues or non-amino acid fragments. Vaccines of the invention  
 CC are produced using 'non-self' peptides synthesised from the  
 CC unnatural D-configuration amino acids to avoid the drawbacks of  
 CC 'self' proteins. The all-D peptides need not be aggregated to be  
 CC operative or immunogenic. They preferably interact with at  
 CC least 1 region of an amyloid protein, e.g. the beta-sheet region  
 CC or GAG-binding site region, the amyloid-beta peptide, or their  
 CC immunogenic fragments, protein conjugates, immunogenic derivative  
 CC peptides and immunogenic peptidomimetics. Examples include all-D  
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,  
 CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D  
 CC derivative peptides given in AAB82623-64. The vaccine elicits a  
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and  
 CC associated cellular toxicity. The amyloid related diseases may be  
 CC localised amyloidosis, e.g. diabetes type II, neurodegenerative  
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob  
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein  
 CC related disorders, or systemic amyloidosis associated with chronic  
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and  
 CC systemic amyloidosis found in long-term haemodialysis patients.

XX Sequence 10 AA;

Query Match 100.0%; Score 55; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 |||||  
 Db 1 hhqklviffaq 10

RESULT 2

AAW01414  
 ID AAW01414 standard; Protein; 28 AA.

XX AC AAW01414;

XX 20-JAN-1997 (first entry)

DE Beta/A4-amyloid peptide residues 1-28 Dutch.

XX Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;  
 KW Alzheimer's disease; stimulation; investigation; pathogenesis;  
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;  
 KW control; cerebral amyloid angiopathy; cerebral; haemorrhage.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 22

FT /note= "wild type Glu substd. with Gln"

XX WO9615799-A1.

XX 30-MAY-1996.

XX

PF 22-NOV-1995; 95WO-US15007.  
 XX  
 PR 22-NOV-1994; 94US-0347144.  
 XX  
 PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

XX Anderson S;

PI WPI; 1996-268332/27.

DR Use of agents which bind beta-amyloid peptide - for diagnosis,  
 PT prevention and treatment of vascular damage caused by amyloid  
 PT deposits, partic. in haemorrhaging and Alzheimer's disease  
 XX  
 PS Example 1; Fig 1; 52pp; English.

XX To investigate the effects of beta-amyloid peptide (BAP) on  
 CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.  
 CC One peptide contained 42 amino acids and corresp. to the full  
 CC length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained  
 CC the 28 N-terminal residues of the BAP found in Alzheimer's disease  
 CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type  
 CC (HCHWA-D), respectively. In an assay to determine the effect of  
 CC the peptides on t-PA activation, each peptide (AAR95248, 49 and 50)  
 CC gave 1st order rate constant of activation (k(app)) values of  
 CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null  
 CC and fibrinogen controls. The results demonstrate that the BAP are  
 CC able to stimulate t-PA activity in vitro, which is significant in  
 CC that it provides a means for investigating and controlling the  
 CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid  
 CC angiopathy related cerebral haemorrhage.

XX Sequence 28 AA;

Query Match 100.0%; Score 55; DB 17; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.00042;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 |||||  
 Db 13 hhqklviffaq 22

RESULT 3

AAB35600

ID AAB35600 standard; peptide; 28 AA.

XX AC AAB35600;

XX 15-FEB-2001 (first entry)

XX Human clone E22Q B(1-28) amyloid B peptide.

KW Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;  
 KW acute cardiovascular disease; therapy.

XX Homo sapiens.

XX US6136548-A.

XX 24-OCT-2000.

XX 02-SEP-1999; 99US-0388890.

XX 26-JUL-1996; 96US-0686959.

XX 22-NOV-1994; 94US-0347144.

XX 22-NOV-1995; 95WO-US15007.

XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

XX Anderson S;

XX

DR WPI; 2001-030939/04.  
 XX Identifying mutant tissue-type plasminogen activator (t-PA) for  
 PT improving thrombolytic therapy or treating vascular hemorrhaging, by  
 PT determining whether t-PA binds to fibrin but not to a beta amyloid  
 PT peptide  
 XX  
 PS Example 3; Column 26; 23pp; English.  
 XX  
 XX The present invention describes a method for identifying mutant  
 CC derivatives of tissue-type plasminogen activator, which involves  
 CC determining whether or not they bind to beta-amyloid peptides and fibrin.  
 CC Mutants will only bind to the latter. These mutants are useful in  
 CC improved thrombolytic therapies, in the treatment of Alzheimer's disease  
 CC and in the treatment of acute cardiovascular disease, which may be caused  
 CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.  
 XX  
 SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 22; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.00042;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 DB 13 HHQKLVFFAQ 22

RESULT 4  
 AAB91803  
 ID AAB91803 standard; Peptide; 35 AA.

XX AAB91803;  
 AC  
 XX  
 XX 22-JUN-2001 (first entry)  
 XX  
 DE Amyloid beta-protein fragment peptide SEQ ID NO:979.  
 XX  
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidy; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

XX WO200069900-A2.  
 XX 23-NOV-2000.  
 XX  
 PF 17-MAY-2000; 2000WO-US13576.  
 XX  
 XX 17-MAY-1999; 99US-0134406.  
 PR 10-SEP-1999; 99US-0153406.  
 PR 15-OCT-1999; 99US-0159783.  
 XX  
 PA (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 XX WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT

PS Disclosure; Page 514; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

SQ Sequence 35 AA;

Query Match 100.0%; Score 55; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 0.00053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 DB 8 HHQKLVFFAQ 17

RESULT 5  
 AAB91830  
 ID AAB91830 standard; Peptide; 35 AA.

XX AAB91830;  
 AC  
 XX  
 XX 22-JUN-2001 (first entry)  
 XX  
 DE Amyloid beta-protein fragment peptide SEQ ID NO:1006.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidy; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

XX WO200069900-A2.  
 XX 23-NOV-2000.  
 XX  
 PF 17-MAY-2000; 2000WO-US13576.  
 XX  
 XX 17-MAY-1999; 99US-0134406.  
 PR 10-SEP-1999; 99US-0153406.  
 PR 15-OCT-1999; 99US-0159783.  
 XX  
 PA (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 XX WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT

PS Disclosure; Page 524; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 55; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 0.00053;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVEFFAQ 10  
 DB 8 hhqklvffaq 17  
 |||||

RESULT 6  
 AAW47232  
 ID AAW47232 standard; peptide; 40 AA.  
 XX AC AAW47232;

XX DT 22-MAY-1998 (first entry)

XX DE Beta-amyloid peptide fragment.

XX KW Screening assay; beta-amyloid peptide; treatment;  
 XX KW amyloidosis disease; Alzheimer's disease.

XX OS Homo sapiens.

XX PN US5721106-A.

XX PD 24-FEB-1998.

XX PF 12-SEP-1994; 94US-0304585.

XX PR 12-SEP-1994; 94US-0304585.

XX PR 13-AUG-1991; 91US-0744767.

XX PA (HARD ) HARVARD COLLEGE.

XX PA (MINU ) UNIV MINNESOTA.

XX PI Maggio JE, Mantyh PW;

XX DR WPI; 1998-168404/15.

XX PT New in vitro screening assay for Alzheimer's disease drugs -  
 PT comprises assessing binding of labelled beta-amyloid peptide to silk  
 PT sample

XX PS Disclosure; Columns 31-32; 36pp; English.

XX CC The present sequence was used in the development of a novel in  
 CC vitro screening assay for agents capable of affecting the  
 CC deposition of beta-amyloid peptide (BAP) on tissue. The method  
 CC comprises contacting a silk sample with labelled BAP, optionally  
 CC in the presence of a test agent, detecting the amount of label  
 CC bound to the silk and assessing the effect of the agent on the  
 CC deposition of BAP. Agents that inhibit binding of BAP to silk are  
 CC potentially useful for treating amyloidosis diseases, especially  
 CC Alzheimer's disease.

XX SQ Sequence 40 AA;

Query Match 100.0%; Score 55; DB 19; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.00062;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHQKLVEFFAQ 10  
 DB 13 hhqklvffaq 22  
 |||||

RESULT 7  
 AAR55697  
 ID AAR55697 standard; Protein; 53 AA.  
 XX AC AAR55697;

XX DT 29-DEC-1994 (first entry)

XX DE Sequence of unidentified protein sequence ID number 22.

XX KW Amyloid precursor protein; APP; plaque; beta/A4; Alzheimers;  
 XX KW transgene; ss.

XX OS Synthetic.

XX PN WO9412627-A.

XX PD 09-JUN-1994.

XX PF 24-NOV-1993; 93WO-US11480.

XX PR 25-NOV-1992; 92US-0989850.

XX PR 09-NOV-1993; 93US-0149222.

XX PA (CEPH-) CEPHALON INC.

XX PI Howland DS, Scott RW;

XX DR WPI; 1994-200256/24.

XX PT Transgenic animal model for Alzheimer's disease - contains  
 PT transgene encoding amyloid protein under transcriptional control  
 PT of synapsin gene promoter

XX PS Example; Page 55; 94pp; English.

XX CC There was no apparent reference to sequence ID numbers 20, 21 or 22  
 CC in the specification. The specification describes a transgenic  
 CC animal model for Alzheimer's disease. A transgenic animal  
 CC harbouring a transgene coding for an amyloid protein under the  
 CC control of a promoter is claimed. The amyloid protein can be  
 CC APP695, APP751 or APP770. The coding sequence may contain a  
 CC mutation, including the hereditary cerebral haemorrhage with  
 CC amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's  
 CC disease (FAD). Perhaps SQ IDs 20-22 corresp. to wt, HCHWA-DT  
 CC and FAD?

XX SQ Sequence 53 AA;

Query Match 100.0%; Score 55; DB 15; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 0.00084;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVEFFAQ 10  
 DB 17 hhqklvffaq 26  
 |||||

RESULT 8  
 AAW26511  
 ID AAW26511 standard; Peptide; 63 AA.  
 XX AC AAW26511;

XX DT 06-JAN-1998 (first entry)



XX Anyloid precursor protein fragment APP-REP 751 (BAP E22Q).

XX Anyloid precursor protein; APP; beta-amyloid protein; BAP;

KW substrate; muten; secretase; Alzheimer's disease;

KW hereditary cerebral haemorrhage with amyloidosis; human.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FT Peptide 10..51

FT /label= BAP(E22Q)

FT /note= "beta-amyloid protein E22Q mutant"

FT Cleavage-site 25..26

FT /note= "secretase cleavage site"

FT Domain 38..61

FT /label= Transmembrane

XX

XX US5656477-A.

PN

XX

XX 12-AUG-1997.

PD

XX

XX 01-MAY-1992; 92US-0877675.

PF

XX

XX 20-SEP-1993; 93US-0123659.

PR

XX

XX 01-MAY-1992; 92US-0877675.

PR

XX

XX (AMCY ) AMERICAN CYANAMID CO.

PA

XX

XX Jacobsen JS, Vitek MP;

PI

XX

XX WPI; 1997-414594/38.

DR

XX

XX Nucleic acid encoding amyloid precursor muten(s) - comprising

PT reporter gene and coding sequence, for identifying compounds which

PT modify the activity of proteolytic enzymes which cleave APP

PT

XX

PS Disclosure; Fig 5A; 84pp; English.

PS

XX

CC This peptide sequence shows the region of amyloid precursor protein

CC (APP) that includes a beta-amyloid protein (BAP) carrying a point

CC mutation (BAP E22Q) found in patients with hereditary cerebral

CC haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an

CC attempt to engineer an APP non-cleavable substrate for secretase,

CC an APP-reporter (APP-REP) protein that carries the E22Q mutation

CC has been expressed in recombinant host cells. This resulted in the

CC secretion of an N-terminal fragment indistinguishable from that of

CC APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be

CC used to detect other putative abnormal APP processing events. They

CC can also be used to investigate cellular post-translational

CC modifications to APP in order to determine the potential influence

CC on normal secretase and abnormal BAP 'clipping' activities.

XX

SQ Sequence 63 AA;

Query Match 100.0%; Score 55; DB 18; Length 63;

Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10

Db |||||

22 hqkklvffa 31

RESULT 9

AAW26391

ID AAW26391 standard; Peptide; 63 AA.

XX

AC AAW26391;

XX

XX 15-DEC-1997 (first entry)

DT

XX

DE Anyloid precursor protein fragment APP-REP 751 (BAP E22Q).

XX

XX Anyloid precursor protein; APP; beta-amyloid protein; BAP;

KW substrate; muten; secretase; Alzheimer's disease;

KW hereditary cerebral haemorrhage with amyloidosis; human.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FT Peptide 10..51

FT /label= BAP(E22Q)

FT /note= "beta-amyloid protein E22Q mutant"

FT Cleavage-site 25..26

FT /note= "secretase cleavage site"

FT Domain 38..61

FT /label= Transmembrane

XX

XX US5652092-A.

PN

XX

XX 29-JUL-1997.

PD

XX

XX 01-MAY-1992; 92US-0877675.

PF

XX

XX 20-SEP-1993; 93US-0123659.

PR

XX

XX 01-MAY-1992; 92US-0877675.

PR

XX

XX 05-JUN-1995; 95US-0462859.

PR

XX

XX (AMCY ) AMERICAN CYANAMID CO.

PA

XX

XX Jacobsen JS, Vitek MP;

PI

XX

XX WPI; 1997-392937/36.

DR

XX

XX Screening for compounds which reduce beta-amyloid protein formation

PT - using cells which express a construct encoding a marker and an

PT amyloid precursor muten derived from APP isoforms

PT

XX

PS Disclosure; Fig 5A; 84pp; English.

PS

XX

CC This peptide sequence shows the region of amyloid precursor protein

CC (APP) that includes a beta-amyloid protein (BAP) carrying a point

CC mutation (BAP E22Q) found in patients with hereditary cerebral

CC haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an

CC attempt to engineer an APP non-cleavable substrate for secretase,

CC an APP-reporter (APP-REP) protein that carries the E22Q mutation

CC has been expressed in recombinant host cells. This resulted in the

CC secretion of an N-terminal fragment indistinguishable from that of

CC APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be

CC used to detect other putative abnormal APP processing events. They

CC can also be used to investigate cellular post-translational

CC modifications to APP in order to determine the potential influence

CC on normal secretase and abnormal BAP 'clipping' activities.

XX

SQ Sequence 63 AA;

Query Match 100.0%; Score 55; DB 18; Length 63;

Best Local Similarity 100.0%; Pred. No. 0.001;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10

Db |||||

22 hqkklvffa 31

RESULT 10

AAW44746

ID AAW44746 standard; Protein; 63 AA.

XX

AC AAW44746;

XX

XX 01-JUN-1998 (first entry)

DT

XX

DE APP-REP 751 [BAP E22Q] peptide.  
 XX Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;  
 KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;  
 KW Alzheimer's disease; cleavage.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Cleavage-site 25..26 "secretase cleavage site"  
 FT  
 FT Misc-difference 31 /note= "Glu to Gln change from wild type sequence"  
 FT  
 XX US5693478-A.  
 XX  
 XX 02-DEC-1997.  
 XX  
 XX 05-JUN-1995; 95US-0464247.  
 XX  
 XX 20-SEP-1993; 93US-0123659.  
 PR 01-MAY-1992; 92US-0877675.  
 PR 05-JUN-1995; 95US-0464247.  
 XX  
 XX (AMCY ) AMERICAN CYANAMID CO.  
 XX  
 XX Jacobsen JS, Vitek MP;  
 PI  
 XX WPI; 1998-031744/03.  
 DR  
 XX Amyloid precursor muten reporter molecule assay containing antibody  
 FT recognised marker - used to study pathways associated with  
 FT Alzheimer's disease  
 PT  
 XX Disclosure; Fig 5A; 84pp; English.  
 PS  
 XX This sequence represents the beta-amyloid protein sequence from the  
 CC construct APP-REP751 [BAP E22Q]. The mutant sequence can be used in a  
 CC method to study secretase and beta-amyloid protein (BAP)-generating  
 CC pathways associated with Alzheimer's disease by studying proteolytic  
 CC cleavage of the reporter polypeptides (e.g. AAW44744 and AAW44745).  
 XX  
 XX Sequence 63 AA;  
 SQ  
 Query Match 100.0%; Score 55; DB 19; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 HHQKLIVFFAQ 10  
 Db 22 hhqklivffaq 31  
 |||||  
 RESULT 11  
 AAW42975  
 ID AAW42975 standard; peptide; 63 AA.  
 XX  
 XX AAW42975;  
 AC  
 XX 01-MAY-1998 (first entry)  
 DT  
 XX Beta-amyloid peptide (BAP) E22Q.  
 DE  
 XX Beta-amyloid peptide; BAP; extracellular BAP plaque; amyloidosis;  
 KW cerebrovascular deposit; Alzheimers disease; Down syndrome;  
 KW Dutch origin; amyloid precursor protein; APP; secretase; BAP aggregation;  
 KW abnormal proteolytic cleavage; hereditary cerebral haemorrhage.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH

FT Domain 38..61  
 FT /note= "putative transmembrane domain"  
 FT Misc\_feature 22  
 FT /label= E22Q  
 FT /note= "wild type Glu replaced with Gln"  
 XX  
 XX US5703209-A.  
 XX  
 XX 30-DEC-1997.  
 XX  
 XX 05-JUN-1995; 95US-0464248.  
 PF  
 XX 20-SEP-1993; 93US-0123659.  
 PR 01-MAY-1992; 92US-0877675.  
 XX  
 XX (AMCY ) AMERICAN CYANAMID CO.  
 XX  
 XX Jacobsen JS, Vitek MP;  
 PI  
 XX WPI; 1998-076482/07.  
 DR  
 XX Amyloid precursor protein fusion polypeptides - comprising APP  
 FT fragment and marker, useful for research and drug screening  
 PT  
 XX Disclosure; Fig 5A; 84pp; English.  
 PS  
 XX The present sequence represents a beta-amyloid peptide (BAP) with a  
 CC E22Q mutation. Abnormal accumulation of extracellular BAP in plaques  
 CC and cerebrovascular deposits is characteristic in brains of individuals  
 CC suffering from Alzheimers disease and Down syndrome. BAP is a poorly  
 CC soluble, self-aggregating protein which is derived from a larger amyloid  
 CC precursor protein (APP). APP is expressed as an integral membrane  
 CC protein, and is cleaved by secretase, between BAP 16lys and 17leu.  
 CC Cleavage at this site precludes amyloidogenesis and results in the  
 CC release of the amino-terminal APP fragment. The E22Q mutation in BAP is  
 CC found within the APP of patients with hereditary cerebral haemorrhage  
 CC with amyloidosis of Dutch origin, and may be due to an alteration in the  
 CC rate of BAP aggregation. APP can be used as a substrate for studying  
 CC abnormal proteolytic cleavage which results in the release of BAP, and  
 CC also to screen for drugs that will inhibit such cleavage.  
 XX  
 XX Sequence 63 AA;  
 SQ  
 Query Match 100.0%; Score 55; DB 19; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0.001;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 HHQKLIVFFAQ 10  
 Db 22 hhqklivffaq 31  
 |||||  
 RESULT 12  
 AAR74695  
 ID AAR74695 standard; Peptide; 99 AA.  
 XX  
 XX AAR74695;  
 AC  
 XX 11-NOV-1995 (first entry)  
 DT  
 XX Beta-amyloid precursor protein mutant C-terminal peptide.  
 DE  
 XX Human; beta-amyloid precursor protein mutant; C-terminal peptide;  
 KW gene transfer; transgenic animal; Alzheimer disease model;  
 KW gene therapy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX EP653154-A.  
 PN  
 XX 17-MAY-1995.  
 PD  
 XX

PF 07-NOV-1994; 94EP-0117512.  
 XX  
 PR 12-NOV-1993; 93JP-0306026.  
 XX  
 PA (FARH ) HOECHST JAPAN LTD.  
 PA (FARH ) HOECHST JAPAN KK.  
 PI  
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;  
 XX  
 XX WPI; 1995-180492/24.  
 DR N-PSDB; AAQ88697.  
 DR  
 XX Transgenic animal model for Alzheimer's disease - contains DNA encoding  
 PT part of beta-amyloid precursor protein in a gene construct designed for  
 PT over-expression in various cell types  
 XX  
 PS Claim 2; Page 13; 32pp; English.  
 XX  
 CC The sequence represents a human brain beta-amyloid precursor protein  
 CC (APP) C-terminal peptide. The peptide is a Gln-22 mutant of  
 CC AAR74694. DNA encoding the peptide may be transferred, along  
 CC with a signal peptide (e.g. AAR74693) gene into somatic and germ  
 CC cells of a non-human mammal, and the resulting transgenic animal  
 CC may be used as a model for Alzheimer disease (AD). The animal  
 CC model exhibits symptoms similar to AD, producing large quantities  
 CC of APP C-terminal peptide, death of neuron cells in pyramidal  
 CC cells at cerebral amyloid regions, increases in glial cells and  
 CC deposition of abnormally phosphorylated tau protein. The animal  
 CC model may be used to develop new therapies for AD, including  
 CC gene therapy strategies.  
 XX  
 SQ Sequence 99 AA;  
 Query Match 100.0%; Score 55; DB 16; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 0.0016;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHQKLVFFAQ 10  
 Db 13 hhqklvffaq 22  
 |||||  
 RESULT 13  
 ID AAB46225  
 AC AAB46225 standard; peptide; 10 AA.  
 AC AAB46225;  
 XX  
 DT 04-APR-2001 (first entry)  
 XX  
 DE Human APP derived immunogenic peptide #21.  
 XX  
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200072880-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 XX 26-MAY-2000; 2000WO-US14810.  
 XX  
 XX 28-MAY-1999; 99US-0322289.  
 PR  
 XX (NEUR-) NEURALAB LTD.  
 PA  
 XX Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 PI  
 XX WPI; 2001-032104/04.  
 DR  
 XX

PT Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid  
 PT specific antibody -  
 XX  
 PS Disclosure; Figure 19; 143pp; English.  
 XX  
 CC This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have neurotropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 94.5%; Score 52; DB 22; Length 10;  
 Best Local Similarity 90.0%; Pred. No. 0.00054;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHQKLVFFAQ 10  
 Db 1 hhqklvffaa 10  
 |||||  
 RESULT 14  
 AAW89358  
 ID AAW89358 standard; peptide; 15 AA.  
 XX  
 AC AAW89358;  
 XX  
 DT 02-MAR-1999 (first entry)  
 XX  
 DE Beta-amyloid peptide derivative A-beta-11-25.  
 XX  
 KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;  
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;  
 KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;  
 KW Creutzfeldt-Jakob disease; bAP.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US5854204-A.  
 XX  
 PD 29-DEC-1998.  
 XX  
 XX 14-MAR-1996; 96US-0612785.  
 PF  
 XX 14-MAR-1996; 96US-0612785.  
 PR  
 PR 14-MAR-1995; 95US-0404831.  
 PR  
 PR 07-JUN-1995; 95US-0475579.  
 PR  
 PR 27-OCT-1995; 95US-0548998.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA  
 XX Benjamin H, Chin J, Findeis MA, Garnick MB, Geftter ML;  
 PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;  
 PI Molineaux S, Nusso G, Reed M, Signer ER, Wakefield J;  
 XX  
 DR WPI; 1999-094964/08.  
 XX  
 XX New peptide(s) derived from beta-amyloid peptide that inhibit  
 PT amyloid aggregation - and neurotoxicity, specifically for treatment  
 PT and prevention of Alzheimer's disease  
 XX

PS Claim 6; Column 81-82; 52pp; English.

CC The present invention describes beta-amyloid peptide (BAP) derivatives.  
CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and  
CC peptides, specifically BAP, and their neurotoxicity, so are useful for  
CC treating and preventing any disease involving amyloidosis, specifically  
CC Alzheimer's disease but also Down's syndrome, familial amyloid  
CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and  
CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose  
CC these diseases, in vitro or in vivo, by detecting binding of BAP to  
CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation  
CC even when BAP is present in molar excess. The present sequence  
CC represents a BAP derivative.

xx Sequence 15 AA;

Query Match 94.5%; Score 52; DB 20; Length 15;  
Best Local Similarity 90.0%; Pred. NO. 0.00084;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
Db |||||:  
3 hhqklvffae 12

RESULT 15

AAR54703  
ID AAR54703 standard; peptide; 17 AA.

XX AC AAR54703;

XX DT 15-DEC-1994 (first entry)

XX DE Beta-amyloid fragment (12-28).

XX KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.

XX OS Homo sapiens.

XX PN WO9409364-A.

XX PD 28-APR-1994.

XX PF 13-OCT-1993; 93WO-US09772.

XX PR 13-OCT-1992; 92US-0959251.

XX PA (UYDU-) UNIV DUKE.

XX PI Strittmatter WJ;

XX DR WPI; 1994-151484/18.

XX PT Immobilised beta-amyloid protein or fragments - used in assays  
PT for obtaining prods for use in the diagnosis and treatment of  
PT disorders such as Alzheimer's disease.

PS Claim 5; Page 28; 49pp; English.

CC A construct comprising a beta-amyloid protein (BAP) or fragment (esp.  
CC the peptides given in AAR54702-03) immobilised on a solid support can be  
CC used to detect cpds. which bind to BAP. Binding of proteins in  
CC human cerebrospinal fluid proteins were shown to bind to beta-  
CC amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28)  
CC was used as control.

xx Sequence 17 AA;

Query Match 94.5%; Score 52; DB 15; Length 17;  
Best Local Similarity 90.0%; Pred. NO. 0.00096;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHQKLVFFAQ 10  
Db |||||:  
2 hhqklvffae 11

Search completed: July 18, 2002, 10:16:10  
Job time: 197 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 18, 2002, 10:14:38 ; Search time 14.76 Seconds  
(without alignments)  
65.101 Million cell updates/sec

Title: US-09-724-842-27  
Perfect score: 55  
Sequence: 1 HHQKLVFFAQ 10

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	52	94.5	42	2 PNO512	beta-amyloid prote
2	52	94.5	57	2 E60045	Alzheimer's diseas
3	52	94.5	57	2 F60045	Alzheimer's diseas
4	52	94.5	57	2 G60045	Alzheimer's diseas
5	52	94.5	57	2 D60045	Alzheimer's diseas
6	52	94.5	57	2 A60045	Alzheimer's diseas
7	52	94.5	57	2 B60045	Alzheimer's diseas
8	52	94.5	82	2 PQ0438	Alzheimer's diseas
9	52	94.5	695	1 A49795	Alzheimer's diseas
10	52	94.5	747	2 JH0773	Alzheimer's diseas
11	52	94.5	770	1 QRU044	Alzheimer's diseas
12	44	80.0	33	2 Z3094	beta-amyloid prote
13	44	80.0	695	2 A27485	Alzheimer's diseas
14	44	80.0	695	2 S00550	Alzheimer's diseas
15	41	74.5	549	1 NUFC	glucose-6-phosphat
16	41	74.5	549	2 H91254	glucosesepphate i
17	41	74.5	549	2 D86095	glucosesepphate i
18	41	74.5	549	2 AD1013	glucose-6-phosphat
19	41	74.5	550	2 B82330	glucose-6-phosphat
20	40	72.7	191	2 T04853	hypothetical prote
21	39	70.9	699	2 H64118	4-alpha-glucanotra
22	38	69.1	272	2 F70979	hypothetical prote
23	38	69.1	549	2 G84996	glucose-6-phosphat
24	37	67.3	635	2 H81793	hypothetical prote
25	36	65.5	210	2 I58391	sarcoma amplified
26	36	65.5	563	2 F64130	glucose-6-phosphat
27	36	65.5	859	2 F69159	protoporphyrin IX
28	36	65.5	1668	1 C69224	cobalamin biosynth
29	35	63.6	297	2 T23909	hypothetical prote

30	35	63.6	446	2 T50786	nucleoid DNA-bind
31	35	63.6	548	2 AF0452	glucose-6-phosphat
32	35	63.6	552	2 T25496	hypothetical prote
33	35	63.6	850	2 JC5047	has GTPase-activat
34	34	61.8	140	2 C81176	hypothetical prote
35	34	61.8	590	2 F95853	probable phospholi
36	34	61.8	763	2 S51300	probable membrane
37	34	61.8	1035	2 T42093	phospholipase D (E
38	34	61.8	1036	2 T13732	phospholipase D (E
39	34	61.8	1036	2 T18530	phospholipase D (E
40	34	61.8	1037	2 T13943	phospholipase D (E
41	34	61.8	1074	2 T17203	phospholipase (EC
42	34	61.8	1074	2 T13725	phospholipase D (E
43	34	61.8	1075	2 T46635	phospholipase D (E
44	34	61.8	1163	2 S07137	DNA-directed RNA p
45	34	61.8	1375	2 T18961	FAB1 protein homol

ALIGNMENTS

RESULT 1  
PNO512  
beta-amyloid protein - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C:Accession: PNO512  
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno  
Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra  
A:Reference number: PNO512; MUID:93290653  
A:Accession: PNO512  
A:Molecule type: protein  
A:Residues: 1-42 <SH1>  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; amyloid

Query Match 94.5%; Score 52; DB 2; Length 42;  
Best Local Similarity 90.0%; Pred. No. 0.0011;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
| | | | | | | | | |  
DB 13 HHQKLVFFAE 22

RESULT 2  
E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C:Species: Ovis sp. (sheep)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: E60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: E60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56130  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;  
Best Local Similarity 90.0%; Pred. No. 0.0015;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
| | | | | | | | | |  
DB 18 HHQKLVFFAE 27

RESULT 3  
F60045  
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: F60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: F60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;  
Best Local Similarity 90.0%; Pred. No. 0.0015;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
| | | | | | | | | |  
Db 18 HHQKLVFFAE 27

RESULT 4  
G60045  
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: G60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: G60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56126  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;  
Best Local Similarity 90.0%; Pred. No. 0.0015;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
| | | | | | | | | |  
Db 18 HHQKLVFFAE 27

RESULT 5  
D60045  
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: D60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: D60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56124  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;  
Best Local Similarity 90.0%; Pred. No. 0.0015;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
| | | | | | | | | |  
Db 18 HHQKLVFFAE 27

RESULT 6  
A60045  
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: A60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: A60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56125  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;  
Best Local Similarity 90.0%; Pred. No. 0.0015;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
| | | | | | | | | |  
Db 18 HHQKLVFFAE 27

RESULT 7  
B60045  
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C:Species: Ursus maritimus (polar bear)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: B60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: B60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;  
Best Local Similarity 90.0%; Pred. No. 0.0015;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
| | | | | | | | | |  
Db 18 HHQKLVFFAE 27

RESULT 8  
PQ0438  
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995  
C:Accession: PQ0438; C60045  
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.  
Biochem. Biophys. Res. Commun. 188, 905-911, 1992  
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs  
A:Reference number: PQ0438; MUID:93075180



A:Accession: PQ0438  
 A:Molecule type: DNA  
 A:Residues: 1-82 <DAV>  
 R:Cross-references: GB:M83558; GB:M83657  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: C60045  
 A:Molecule type: mRNA  
 A:Residues: 12-68 <JOH>  
 A:Cross-references: EMBL:X56129  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 94.5%; Score 52; DB 2; Length 82;  
 Best Local Similarity 90.0%; Pred. No. 0.0022;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10  
 |||||  
 Db 29 HHOKLVFFAE 38

RESULT 9  
 A49795  
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C:Species: Macaca fascicularis (crab-eating macaque)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A49795  
 R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.  
 Am. J. Pathol. 138, 1423-1435, 1991  
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
 A:Reference number: A49795; MUID:91273117  
 A:Accession: A49795  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <POD>  
 C:Cross-references: GB:M58727; NID:G342062; PIDN:AAA36829.1; PID:G342063  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing

Query Match 94.5%; Score 52; DB 1; Length 695;  
 Best Local Similarity 90.0%; Pred. No. 0.021;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10  
 |||||  
 Db 609 HHOKLVFFAE 618

RESULT 10  
 JH0773  
 Alzheimer's disease amyloid beta protein precursor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
 C:Accession: JH0773  
 R:Okado, H.; Okamoto, H.  
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental  
 A:Reference number: JH0773; MUID:93129227  
 A:Accession: JH0773  
 A:Molecule type: mRNA  
 A:Residues: 1-747 <OKA>  
 A:Cross-references: GB:S52417; NID:G263150; PIDN:AAB24853.1; PID:G263151  
 A:Experimental source: larva  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid  
 F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 94.5%; Score 52; DB 2; Length 747;  
 Best Local Similarity 90.0%; Pred. No. 0.023;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10  
 |||||  
 Db 661 HHOKLVFFAE 670

RESULT 11  
 ORHU44  
 Alzheimer's disease amyloid beta protein precursor [validated] - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIA Inh  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39453; I39454; I39455;  
 4658; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252;  
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;  
 Nucleic Acids Res. 17, 517-522, 1989  
 A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEM1>  
 A:Cross-references: EMBL:X13466  
 A>Note: alternative splice form APP(695)  
 R:Lemaire, H.G.  
 submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:G871360  
 A>Note: alternative splice form APP(695)  
 R:La Fauti, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAP>  
 A:Cross-references: GB:M24546; GB:M24547; NID:G341202; PIDN:AAC13654.1; PID:G516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila  
 A:Reference number: A33260; MUID:89392030  
 A:Accession: A33260  
 A:Molecule type: DNA  
 A:Residues: 656-737 <JOH>  
 A:Cross-references: GB:M29270; NID:G178863; PIDN:AAA51768.1; PID:G178865  
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid  
 A:Reference number: A35486; MUID:90321244  
 A:Accession: A35486  
 A:Molecule type: DNA  
 A:Residues: 672-710 <PRE1>  
 A>Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
 R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuwa, H.; Sakaki, Y.  
 Gene 87, 257-263, 1990  
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
 A:Reference number: I39451; MUID:90236318  
 A:Accession: I39451  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-770 <YOS1>  
 A:Cross-references: GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:G178616  
 A:Accession: I39451  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>

A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615  
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 102, 291-292, 1991  
A:Contents: annotation; erratum  
A:Note: revised physical map for reference I39451  
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine  
Science 248, 1124-1126, 1990  
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh  
A:Reference number: I39453; MUID:90260663  
A:Accession: I39453  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 636-737 <LEV>  
A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620  
A:Note: a mutation with 693-Gln is presented  
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
Science 254, 97-99, 1991  
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer  
A:Reference number: I59362; MUID:92022553  
A:Accession: I59362  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 689-716, 'F', 718-737 <MUR>  
A:Cross-references: GB:M57665; NID:g236720; PIDN:AAB19991.1; PID:g236721  
R:Kamino, K.; Orr, H.R.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,  
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,  
Am. J. Hum. Genet. 51, 998-1014, 1992  
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the  
A:Reference number: A44017; MUID:93035397  
A:Accession: A44017  
A:Molecule type: DNA  
A:Residues: 687-692, 'G', 694-718 <KAM1>  
A:Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378  
A:Experimental source: familial Alzheimer disease family SB  
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)  
A:Accession: B44017  
A:Molecule type: DNA  
A:Residues: 687-718 <KAN2>  
A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380  
A:Experimental source: familial Alzheimer disease family LIT  
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)  
A:Note: this sequence has a silent mutation  
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
Nature 325, 733-736, 1987  
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac  
A:Reference number: A03134; MUID:87144572  
A:Accession: A03134  
A:Molecule type: mRNA  
A:Residues: 1-288, 'V', 365-770 <KAN>  
A:Cross-references: GB:F00364; NID:g28525; PIDN:CAA68374.1; PID:g28526  
A:Note: alternative splice form APP(695)  
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a  
A:Reference number: A29030; MUID:87231971  
A:Accession: A29030  
A:Molecule type: mRNA  
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540  
A:Note: the authors translated the codon GAG for residue 647 as ASP  
R:Goldgraber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.  
Science 235, 877-880, 1987  
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
A:Reference number: A47584; MUID:87120328  
A:Accession: A47584  
A:Molecule type: mRNA  
A:Residues: 674-756, 'S', 758-770 <GOL>  
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707  
A:Experimental source: brain  
R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
Science 235, 880-884, 1987  
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th

A:Reference number: A47585; MUID:87120329  
A:Accession: A47585  
A:Molecule type: mRNA  
A:Residues: 674-703 <TAN1>  
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958  
R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue  
EMBO J. 7, 949-957, 1988  
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p  
A:Reference number: S02638; MUID:88296437  
A:Accession: S02638  
A:Molecule type: mRNA  
A:Residues: 672-678 <DYK>  
R:Tanzil, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N  
Nature 331, 528-530, 1988  
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc  
A:Reference number: S00707; MUID:88122640  
A:Accession: S00707  
A:Molecule type: mRNA  
A:Residues: 286-344, 'I', 365-366 <TAN2>  
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612  
A:Experimental source: promyelocytic leukemia cell line HL60  
A:Note: alternative splice form APP(751)  
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;  
Nature 331, 525-527, 1988  
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh  
A:Reference number: S00925; MUID:88122639  
A:Accession: S00925  
A:Molecule type: mRNA  
A:Residues: 1-344, 'I', 365-770 <PO>  
A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721  
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
Nature 331, 530-532, 1988  
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi  
A:Reference number: A38949; MUID:88122641  
A:Accession: A38949  
A:Molecule type: mRNA  
A:Residues: 287-367 <KIT>  
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611  
A:Experimental source: glioblastoma cell line  
A:Note: alternative splice form APP(770)  
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash  
Brain Res. Mol. Brain Res. 4, 121-131, 1988  
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre  
A:Reference number: A30320  
A:Accession: A30320  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 284-288, 'V', 365-770 <VIT1>  
A:Accession: B30320  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 122-288, 'V', 365-770 <VIT2>  
A:Accession: C30320  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 606-770 <VIT3>  
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,  
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease  
A:Reference number: A31087; MUID:88124954  
A:Accession: A31087  
A:Molecule type: mRNA  
A:Residues: 507-770 <ZAI>  
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573  
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue  
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue  
A:Note: the cited Genbank accession number, J03594, is not in release 101.0  
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther,

Query Match 94.5%; Score 52; DB 1; Length 770;  
Best Local Similarity 90.08; Pred. No. 0.023;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 |||||  
 Db 684 HHQKLVFFAE 693

## RESULT 12

S23094  
 beta-amyloid protein precursor - rat  
 N;Alternate names: Rattus norvegicus (Norway rat)  
 C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
 C;Accession: S23094  
 R;Kojima, S.; Omori, M.  
 FEBS Lett. 304, 57-60, 1992  
 A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
 A;Reference number: S23094; MUID:92316198  
 A;Accession: S23094  
 A:Molecule type: protein  
 A;Residues: 1-33 <KOJ>  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 80.0%; Score 44; DB 2; Length 33;  
 Best Local Similarity 88.9%; Pred. No. 0.035;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHQKLVFFAQ 10  
 |||||  
 Db 19 HHQKLVFFAE 27

## RESULT 13

A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N;Alternate names: proteinase nexin II  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
 C;Accession: A27485; S19727; I49485  
 R;Yamada, T.; Sakaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor  
 A;Reference number: A27485; MUID:88106489  
 A;Accession: A27485  
 A:Molecule type: mRNA

A;Residues: 1-695 <YAM>  
 A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085  
 A;Experimental source: brain  
 R;de Strooper, B.; van Leuven, F.; van den Berghe, H.  
 Biochim. Biophys. Acta 1129, 141-143, 1991  
 A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
 A;Reference number: S19727; MUID:92096458  
 A;Accession: S19727

A:Molecule type: mRNA  
 A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
 A;Cross-references: EMBL:X59379  
 R;Izumii, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
 Gene 112, 189-195, 1992  
 A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
 A;Reference number: I49485; MUID:92209998  
 A;Accession: I49485

A;Status: translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A;Residues: 1-19 <RES>  
 A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329  
 C;Genetics:  
 A;Map position: 16C3  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 80.0%; Score 44; DB 2; Length 695;  
 Best Local Similarity 88.9%; Pred. No. 0.84;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHQKLVFFAQ 10  
 |||||  
 Db 610 HHQKLVFFAE 618

## RESULT 14

S00550  
 Alzheimer's disease amyloid beta protein precursor - rat  
 N;Alternate names: beta-A4 amyloid protein  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
 C;Accession: S00550; A41245; A39820; S46251  
 R;Shivers, B.D.; Hibich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
 EMBO J. 7, 1365-1370, 1988  
 A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
 A;Reference number: S00550; MUID:88312583  
 A;Accession: S00550

A:Molecule type: mRNA  
 A;Residues: 1-695 <SHI>  
 A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617  
 R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.  
 Science 241, 223-226, 1988  
 A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
 A;Reference number: A41245; MUID:88264430  
 A;Accession: A41245

A:Molecule type: protein  
 A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
 A;Note: evidence for heparan sulfate attachment  
 R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.  
 FEBS Lett. 349, 109-116, 1994  
 A;Title: The beta-A4 amyloid precursor protein binding to copper.  
 A;Reference number: S46251; MUID:94320627  
 A;Contents: annotation; copper binding sites  
 A;Note: rat peptides were isolated but not sequenced  
 R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
 J. Biol. Chem. 266, 8464-8469, 1991

A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
 A;Reference number: A39820; MUID:91217087  
 A;Accession: A39820  
 A;Status: preliminary  
 A:Molecule type: protein  
 A;Residues: 18-32 <POT>

A;Experimental source: brain  
 C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteins  
 C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
 F;625-648/Domain: transmembrane #status predicted <TMM>

Query Match 80.0%; Score 44; DB 2; Length 695;  
 Best Local Similarity 88.9%; Pred. No. 0.84;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHQKLVFFAQ 10  
 |||||  
 Db 610 HHQKLVFFAE 618

## RESULT 15

NUEC  
 glucose-6-phosphate isomerase (EC 5.3.1.9) - Escherichia coli  
 N;Alternate names: phosphoglucose isomerase; phosphohexose isomerase  
 C;Species: Escherichia coli  
 C;Date: 31-Mar-1990 #sequence\_revision 17-Oct-1997 #text\_change 08-Sep-2000  
 C;Accession: H65209; J50142; S04396  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617  
 A;Accession: H65209  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA  
A: Residues: 1-549 <BLAT>  
A: Cross-references: GB:AF000476; GB:U00096; NID:gl790456; PIDN:AAC76995.1; PID:gl790457;  
A: Experimental source: strain K-12, substrain MG1655  
R: Froman, B.E.; Tait, R.C.; Gottlieb, L.D.  
Mol. Gen. Genet. 217, 126-131, 1989  
A: Title: Isolation and characterization of the phosphoglucose isomerase gene from Escherichia coli  
A: Reference number: JS0142; MUID:89364675  
A: Accession: JS0142  
A: Molecule type: DNA  
A: Residues: 1-316,'V',318-549 <PRO>  
A: Cross-references: GB:X15196; NID:g42376; PIDN:CAA33268.1; PID:g42377  
A: Experimental source: Strain JM101  
A: Note: the authors translated the codon CAG for residue 8 as Trp  
C: Comment: This enzyme catalyzes the reversible isomerization of glucose-6-phosphate and fructose-6-phosphate  
C: Genetics:  
A: Gene: pg1  
A: Map position: 91 min  
A: Superfamily: glucose-6-phosphate isomerase  
C: Keywords: glycolysis; homodimer; intramolecular oxidoreductase; isomerase  
F:514/Active site: Lys #status predicted

Query Match 74.5%; Score 41; DB 1; Length 549;  
Best Local Similarity 75.0%; Pred. No. 2.6;  
Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;  
Qy 1 HHOKLV--FFAQ 10  
Db 416 HHQKLSNFFAQ 427  
||||| |||||

Search completed: July 18, 2002, 10:16:51  
Job time: 133 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:16:33 ; Search time 10.34 Seconds  
(without alignments)  
37.446 Million cell updates/sec

Title: US-09-724-842-27  
Perfect score: 55  
Sequence: 1 HHOKLVFFAQ 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	94.5	57	1 A4_PIG	Q29023 sus scrofa
2	52	94.5	57	1 A4_URMA	Q29149 ursus marit
3	52	94.5	58	1 A4_CANFA	Q28280 canis famli
4	52	94.5	58	1 A4_RABIT	Q28748 oryctolagus
5	52	94.5	59	1 A4_SHEEP	Q28757 ovis aries
6	52	94.5	58	1 A4_BOVIN	Q28053 bos taurus
7	52	94.5	751	1 A4_SAISC	Q95241 salmisi sci
8	52	94.5	770	1 A4_HUMAN	P05067 homo sapien
9	44	80.0	770	1 A4_MOUSE	P12023 mus musculu
10	44	80.0	770	1 A4_RAT	P08592 rattus norv
11	41	74.5	549	1 G6PI_ECOLI	P11537 escherichia
12	41	74.5	550	1 G6PI_VIBCH	Q9kuy4 vibrio chol
13	39	70.9	699	1 MALQ_HAEIN	P45176 haemophilus
14	38	69.1	549	1 G6PI_BUCAL	P57636 buchnera ap
15	38	69.1	549	1 G6PI_PASMU	Q9cml2 pasteurella
16	36	65.5	109	1 SAS_PIG	Q29257 sus scrofa
17	36	65.5	204	1 TNS6_HUMAN	Q95857 homo sapien
18	36	65.5	210	1 SAS_HUMAN	Q12999 homo sapien
19	36	65.5	549	1 G6PI_HAEIN	P44312 klebsiella
20	35	63.6	167	1 G6PI_KLEOX	P77877 klebsiella
21	35	63.6	849	1 RSG2_HUMAN	Q15283 homo sapien
22	34	61.8	763	1 YNS1_YEAST	P42843 saccharomyc
23	34	61.8	1036	1 PLD1_CRIGR	O08684 cricetus
24	34	61.8	1074	1 PLD1_HUMAN	Q13393 homo sapien
25	34	61.8	1074	1 PLD1_MOUSE	Q92280 mus musculu
26	34	61.8	1074	1 PLD1_RAT	P70496 rattus norv
27	34	61.8	1163	1 RPOD_PEA	P12227 pisum sativ
28	34	61.8	4427	1 PKSL_BACSU	Q05470 bacillus su
29	33	60.0	214	1 ACUB_BACSU	P39066 bacillus su
30	33	60.0	278	1 IOD3_HUMAN	P55073 homo sapien
31	33	60.0	278	1 IOD3_RAT	P49897 rattus norv
32	33	60.0	325	1 ILOS_HUMAN	Q08334 homo sapien
33	33	60.0	346	1 ILVC_BUCUE	Q9a97 buchnera ap

34	33	60.0	421	1 HUTI_BACSU	P42084 bacillus su
35	33	60.0	482	1 PO24_POPJA	Q03275 popillia ja
36	33	60.0	496	1 C7D9_SOYBN	O81971 glycine max
37	33	60.0	564	1 SYT_MYCGE	P47615 mycoplasma
38	33	60.0	754	1 CHLD_PEA	O22437 pisum sativ
39	33	60.0	758	1 CHLD_TOBAC	O24133 nicotiana t
40	33	60.0	759	1 CHLD_ARATH	O9S91 arabidopsis
41	32	58.2	124	1 SLP_BACSU	P39910 bacillus su
42	32	58.2	321	1 CYP_GUITH	O78494 guillardia
43	32	58.2	332	1 RPSB_ANASP	Q03065 anabaena sp
44	32	58.2	380	1 FD3E_SOYBN	P48625 glycine max
45	32	58.2	462	1 MPPB_YEAST	P10507 saccharomyc

ALIGNMENTS

RESULT 1					
ID A4_PIG		STANDARD;	PRT;	57 AA.	
AC Q29023;					
DT 01-NOV-1997 (Rel. 35, Created)					
DT 01-NOV-1997 (Rel. 35, Last sequence update)					
DT 16-OCT-2001 (Rel. 40, Last annotation update)					
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid					
DE protein (Beta-APP) (A-beta)] (Fragment).					
DE APP.					
OS Sus scrofa (Pig).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.					
OX NCBI_TaxID=9823;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Brain;					
RX MEDLINE=92017079; PubMed=1656157;					
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;					
RT "Conservation of the sequence of the Alzheimer's disease amyloid					
RT peptide in dog, polar bear and five other mammals by cross-species					
RT polymerase chain reaction analysis.";					
RL Brain Res. Mol. Brain Res. 10:299-305(1991).					
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO					
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN					
CC G(O) (BY SIMILARITY).					
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.					
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration					
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CC or send an email to license@isb-sib.ch).					
CC -----					
CC EMBL; X56127; CAA39592.1; -.					
DR HSSP; P05067; IBA4.					
DR InterPro; IPR001868; A4_APP.					
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.					
DR PROSITE; PS00320; A4_INTRA; PARTIAL.					
KW Glycoprotein; Amyloid; Neurone; Transmembrane.					
FT NON_TER 1 1					
FT CHAIN 6 48					
FT DOMAIN <1 33					
FT TRANSMEM 34 57					
FT NON_TER 57 57					
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;					

Query Match 94.5%; Score 52; DB 1; Length 57;  
Best Local similarity 90.0%; Pred. No. 0.00081;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10

|||||  
18 HHQKLVEFAE 27

## RESULT 2

A4\_URSGMA STANDARD; PRT; 57 AA.  
ID A4\_URSGMA  
AC Q29149;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
DE protein (Beta-APP) (A-beta)] (Fragment).  
GN APP.  
OS Ursus maritimus (Polar bear) (Thalarchos maritimus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
OX NCBI\_TaxID=29073;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
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CC  
CC EMBL; X56128; CAA39593.1; -  
CC HSPSP; P05067; 1AML.  
CC InterPro; IPR001868; A4\_APP.  
CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
FT NON\_TER 1 1  
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 34 57 POTENTIAL.  
FT NON\_TER 57 57  
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 94.5%; Score 52; DB 1; Length 57;  
Best Local Similarity 90.0%; Pred. No. 0.00081;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHQKLVEFAQ 10  
| | | | | | | | | |

Db 18 HHQKLVEFAE 27

## RESULT 3

A4\_CANFA STANDARD; PRT; 58 AA.  
ID A4\_CANFA  
AC Q28280;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
DE protein (Beta-APP) (A-beta)] (Fragment).  
GN APP.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
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CC  
CC EMBL; X56128; CAA39593.1; -  
CC HSPSP; P05067; 1AML.  
CC InterPro; IPR001868; A4\_APP.  
CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
FT NON\_TER 1 1  
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 34 57 POTENTIAL.  
FT NON\_TER 57 57  
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Oy 1 HHQKLVEFAQ 10  
| | | | | | | | | |

Db 18 HHQKLVEFAE 27

GN APP.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
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CC  
CC EMBL; X56125; CAA39590.1; -  
CC HSPSP; P05067; 1BM4.  
CC InterPro; IPR001868; A4\_APP.  
CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
FT NON\_TER 1 1  
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 35 58 POTENTIAL.  
FT NON\_TER 58 58  
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 94.5%; Score 52; DB 1; Length 58;  
Best Local Similarity 90.0%; Pred. No. 0.00082;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHQKLVEFAQ 10  
| | | | | | | | | |

Db 19 HHQKLVEFAE 28

## RESULT 4

A4\_RABIT STANDARD; PRT; 58 AA.  
ID A4\_RABIT  
AC Q28748;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
DE protein (Beta-APP) (A-beta)] (Fragment).  
GN APP.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
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CC  
CC EMBL; X56128; CAA39593.1; -  
CC HSPSP; P05067; 1AML.  
CC InterPro; IPR001868; A4\_APP.  
CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
FT NON\_TER 1 1  
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 35 58 POTENTIAL.  
FT NON\_TER 58 58  
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 94.5%; Score 52; DB 1; Length 58;  
Best Local Similarity 90.0%; Pred. No. 0.00082;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHQKLVEFAQ 10  
| | | | | | | | | |

Db 19 HHQKLVEFAE 28

RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -|- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.  
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CC  
CC EMBL; X56129; CAA39594.1; -.  
CC HSSP; P05067; 1BA4.  
CC InterPro; IPR001868; A4\_APP.  
CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
CC Glycoprotein; Amyloid; Neurone; Transmembrane.  
CC NON\_TER 1 1  
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 34 57 POTENTIAL.  
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
CC NON\_TER 58 58  
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;  
CC  
CC Query Match 94.5%; Score 52; DB 1; Length 58;  
CC Best Local Similarity 90.0%; Pred. No. 0.00082;  
CC Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 HHOKLVFFAQ 10  
CC | | | | | | | | | |  
CC Db 18 HHOKLVFFAE 27  
CC  
CC RESULT 5  
CC A4\_SHEEP  
CC ID A4\_SHEEP STANDARD; PRT; 58 AA.  
CC Q28757;  
CC DT 01-NOV-1997 (Rel. 35, Created)  
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)  
CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
CC protein (Beta-APP) (A-beta)] (Fragment).  
CC GN APP.  
CC OS Ovis aries (Sheep).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
CC OC Bovidae; Caprinae; Ovis.  
CC OX NCBI\_TaxID=9940;  
CC RN [1]  
CC RP SEQUENCE FROM N.A.  
CC RC TISSUE=Heart;  
CC RX MEDLINE=92017079; PubMed=1656157;  
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
CC "Conservation of the sequence of the Alzheimer's disease amyloid  
CC peptide in dog, polar bear and five other mammals by cross-species  
CC polymerase chain reaction analysis.";  
CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -|- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.  
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CC  
CC EMBL; X56130; CAA39595.1; -.  
CC HSSP; P05067; 1AML.  
CC InterPro; IPR001868; A4\_APP.  
CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
CC Glycoprotein; Amyloid; Neurone; Transmembrane.  
CC NON\_TER 1 1  
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 34 57 POTENTIAL.  
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
CC NON\_TER 58 58  
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;  
CC  
CC Query Match 94.5%; Score 52; DB 1; Length 58;  
CC Best Local Similarity 90.0%; Pred. No. 0.00082;  
CC Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 HHOKLVFFAQ 10  
CC | | | | | | | | | |  
CC Db 18 HHOKLVFFAE 27  
CC  
CC RESULT 6  
CC A4\_BOVIN  
CC ID A4\_BOVIN STANDARD; PRT; 59 AA.  
CC Q28053;  
CC DT 01-NOV-1997 (Rel. 35, Created)  
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)  
CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
CC protein (Beta-APP) (A-beta)] (Fragment).  
CC GN APP.  
CC OS Bos taurus (Bovine).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
CC OC Bovidae; Bovinae; Bos.  
CC OX NCBI\_TaxID=9913;  
CC RN [1]  
CC RP SEQUENCE FROM N.A.  
CC RC TISSUE=Brain;  
CC RX MEDLINE=92017079; PubMed=1656157;  
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
CC "Conservation of the sequence of the Alzheimer's disease amyloid  
CC peptide in dog, polar bear and five other mammals by cross-species  
CC polymerase chain reaction analysis.";  
CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -|- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X56124; CAA39589.1; -.  
CC EMBL; X56126; CAA39591.1; -.  
CC HSSP; P05067; 1BA4.  
CC InterPro; IPR001868; A4\_APP.  
CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
CC Glycoprotein; Amyloid; Neurone; Transmembrane.  
CC NON\_TER 1 1  
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 34 57 POTENTIAL.  
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
CC NON\_TER 58 58  
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;  
CC  
CC Query Match 94.5%; Score 52; DB 1; Length 58;  
CC Best Local Similarity 90.0%; Pred. No. 0.00082;  
CC Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 HHOKLVFFAQ 10  
CC | | | | | | | | | |  
CC Db 18 HHOKLVFFAE 27  
CC  
CC RESULT 6  
CC A4\_BOVIN  
CC ID A4\_BOVIN STANDARD; PRT; 59 AA.  
CC Q28053;  
CC DT 01-NOV-1997 (Rel. 35, Created)  
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)  
CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
CC protein (Beta-APP) (A-beta)] (Fragment).  
CC GN APP.  
CC OS Bos taurus (Bovine).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
CC OC Bovidae; Bovinae; Bos.  
CC OX NCBI\_TaxID=9913;  
CC RN [1]  
CC RP SEQUENCE FROM N.A.  
CC RC TISSUE=Brain;  
CC RX MEDLINE=92017079; PubMed=1656157;  
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
CC "Conservation of the sequence of the Alzheimer's disease amyloid  
CC peptide in dog, polar bear and five other mammals by cross-species  
CC polymerase chain reaction analysis.";  
CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -|- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X56124; CAA39589.1; -.  
CC EMBL; X56126; CAA39591.1; -.  
CC HSSP; P05067; 1BA4.  
CC InterPro; IPR001868; A4\_APP.  
CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
CC Glycoprotein; Amyloid; Neurone; Transmembrane.  
CC NON\_TER 1 1  
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 34 57 POTENTIAL.  
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
CC NON\_TER 58 58  
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;  
CC  
CC Query Match 94.5%; Score 52; DB 1; Length 58;  
CC Best Local Similarity 90.0%; Pred. No. 0.00082;  
CC Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 HHOKLVFFAQ 10  
CC | | | | | | | | | |  
CC Db 18 HHOKLVFFAE 27  
CC  
CC RESULT 6  
CC A4\_BOVIN  
CC ID A4\_BOVIN STANDARD; PRT; 59 AA.  
CC Q28053;  
CC DT 01-NOV-1997 (Rel. 35, Created)  
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)  
CC DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
CC protein (Beta-APP) (A-beta)] (Fragment).  
CC GN APP.  
CC OS Bos taurus (Bovine).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
CC OC Bovidae; Bovinae; Bos.  
CC OX NCBI\_TaxID=9913;  
CC RN [1]  
CC RP SEQUENCE FROM N.A.  
CC RC TISSUE=Brain;  
CC RX MEDLINE=92017079; PubMed=1656157;  
CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
CC "Conservation of the sequence of the Alzheimer's disease amyloid  
CC peptide in dog, polar bear and five other mammals by cross-species  
CC polymerase chain reaction analysis.";  
CC RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -|- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC  
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FT NON_TER 1 1
FT CHAIN 7 49
FT DOMAIN <1 34 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 35 58 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 59 >59 POTENTIAL.
FT NON_TER 59 59 CYTOPLASMIC (POTENTIAL).
FT SEQUENCE 59 AA: 6414 MW: 434690488A2E12D CRC64;

Query Match 94.5%; Score 52; DB 1; Length 59;
Best Local Similarity 90.0%; Pred. No. 0.00084;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
Db 19 HHQKLVFFAE 28

RESULT 7
A4_SNAISC
ID A4_SNAISC STANDARD; PRT; 751 AA.
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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HMBL; S81024; NAD14347.1;
HSSP; P05067; JAAP
DR InterPro; IPR001868; A4_APP.
DR Pfam; P000223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing; Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA: 84893 MW: 6C3E431089569049 CRC64;
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Query Match 94.5%; Score 52; DB 1; Length 751;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
Db 665 HHQKLVFFAE 674
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RESULT 8
A4_HUMAN
ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APPI) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP OR A4 OR CVAP OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.";
RT Nature 325:733-736(1987).
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.";
RT Nature 331:525-527(1988).
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
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RA Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for  
 RT sequencing of a 300 kb region of human APP locus.";  
 RL Nucleic Acids Res. 25:1802-1808(1997).  
 RN [5]  
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
 RX MEDLINE-88122640; PubMed-2893290;  
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
 RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease.";  
 RL Nature 331:528-530(1988).  
 RN [6]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE-88122641; PubMed-2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RT protease inhibitory activity.";  
 RL Nature 331:530-532(1988).  
 RN [7]  
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE-87231971; PubMed-3035574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RN [8]  
 RP SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE-88124954; PubMed-2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [9]  
 RP SEQUENCE OF 672-681.  
 RX MEDLINE-88035004; PubMed-3312495;  
 RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tourtellotte W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RT microvessels.";  
 RL J. Neurochem. 49:1394-1401(1987).  
 RN [10]  
 RP SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE-90236318; PubMed-2110105;  
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene.";  
 RL Gene 87:257-263(1990).  
 RN [11]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RX TISSUE-Liver;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide.";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [12]  
 RP SEQUENCE OF 18-50.  
 RX MEDLINE-87250462; PubMed-3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts.";  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [13]  
 RP IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE-89384866; PubMed-2506449;  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RT the Kunitz domain is protease nexin-II.";

RL Nature 341:144-147(1989).  
 RN [14]  
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE-90211252; PubMed-1969731;  
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
 RT disease amyloid protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
 RN [15]  
 RP COMPLEX WITH G(O).  
 RX MEDLINE-93188965; PubMed-8446172;  
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RT protein G(O).";  
 RL Nature 362:75-79(1993).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE-99215582; PubMed-10201399;  
 RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RT Alzheimer amyloid precursor protein.";  
 RL Nat. Struct. Biol. 6:327-331(1999).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE-91104913; PubMed-2125487;  
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;  
 RT "X-ray crystal structure of the protease inhibitor domain of  
 RT Alzheimer's amyloid beta-protein precursor.";  
 RL Biochemistry 23:10018-10022(1990).  
 RN [18]  
 RP STRUCTURE BY NMR OF 289-344.  
 RX MEDLINE-92031488; PubMed-1718421;  
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,  
 RA Kamarcik M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
 RA Tamburini P.P.;  
 RT "Sequential NMR resonance assignment and structure determination of  
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
 RT precursor protein.";  
 RL Biochemistry 30:10467-10478(1991).  
 RN [19]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE-94281210; PubMed-7516706;  
 RA Talafous J., Marcinkowski K.J., Klopman G., Zagorski M.G.;  
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";  
 RL Biochemistry 33:7788-7796(1994).  
 RN [20]  
 RP STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE-97128622; PubMed-8973180;  
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
 RT membrane-mimicking environment.";  
 RL Biochemistry 35:16094-16104(1996).  
 RN [21]  
 RP STRUCTURE BY NMR OF 672-711.  
 RX MEDLINE-98359783; PubMed-9693002;  
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle  
 RT environment. Is the membrane-spanning domain where we think it is?";  
 RL Biochemistry 37:11064-11077(1998).  
 RN [22]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE-20400056; PubMed-10940222;  
 RA Poulsen S.-A., Watson A.A., Craik D.J.;  
 RT "Solution structures in aqueous SDS micelles of two amyloid beta  
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
 RT site.";  
 RL J. Struct. Biol. 130:142-152(2000).  
 RN [23]  
 RP STRUCTURE BY NMR OF 681-706.  
 RX MEDLINE-20400055; PubMed-10940221;

RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,  
 RA Lu Y., Felix A.M., Magglio J.E., Lee J.P.;  
 RA "The Alzheimer's peptide a beta adopts a collapsed coil structure in  
 RA water.";  
 RL J. Struct. Biol. 130:130-141(2000).  
 RN [24]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.  
 RX MEDLINE=88296437; PubMed=2900137;  
 RA Dykx T., Weidmann A., Muthaup G., Salbaum J.M., Lemaire H.-G.,  
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;  
 RT "Identification, transmembrane orientation and biogenesis of the  
 RT amyloid A4 precursor of Alzheimer's disease.";  
 RN [5]  
 QY Query Match 94.5%; Score 52; DB 1; Length 770;  
 Best Local Similarity 90.0%; Pred. No. 0.011;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 684 HHQKLVFFAE 693  
 1 HHQKLVFFAQ 10  
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 RESULT 9  
 A4\_MOUSE  
 ID A4\_MOUSE STANDARD; PRT; 770 AA.  
 AC P12023;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog precursor  
 DE (Amyloidogenic glycoprotein) (AG).  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Brain;  
 RX MEDLINE=92096458; PubMed=1756177;  
 RA de Strooper B., van Leuven F., van den Bergh H.;  
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse  
 RT is closer related to its human homolog than previously reported.";  
 RL Biochim. Biophys. Acta 1129:141-143(1991).  
 RN [2]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=88106489; PubMed=3322280;  
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;  
 RT "Complementary DNA for the mouse homolog of the human amyloid beta  
 RT protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
 RN [3]  
 RP REVISIONS.  
 RA Yamada T.;  
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC STRAIN=CD-1; TISSUE=Placenta;  
 RX MEDLINE=89345111; PubMed=2569710;  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of Mus domesticus.";  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE=9209998; PubMed=1555768;  
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
 RA Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
 RL Gene 112:189-195(1992).  
 RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Brain, and Kidney;  
 RX MEDLINE=89149813; PubMed=2493250;  
 RA Yanada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;  
 RT "Structure and expression of the alternatively-spliced forms of mRNA  
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
 RT precursor.";  
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),  
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS  
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND  
 CC LIVER.  
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
 CC PHOSPHORYLATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC -----  
 CC EMBL; X59379; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; M18373; AAA37139.1; -;  
 DR EMBL; X15210; CAA33280.1; -;  
 DR EMBL; D10603; BAA01456.1; -;  
 DR EMBL; M24397; AAA39929.1; -;  
 DR PIR; A27485; A27485.  
 DR PIR; S04855; S04855.  
 DR PIR; S19727; S19727.  
 DR HSSP; P05067; 10CM.  
 DR MGD; MGI:88059; APP.  
 DR InterPro; IPR001868; A4\_APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 1.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17  
 FT CHAIN 18 770  
 FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN  
 FT HOMOLOG.  
 FT DOMAIN 18 699  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 700 723  
 FT POTENTIAL.  
 FT DOMAIN 724 770  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 673 715  
 FT EQUIVALENT OF BETA-AMYLOID PROTEIN.  
 FT DOMAIN 287 345  
 FT BPTI/KUNITZ INHIBITOR.  
 FT SITE 759 762  
 FT CLATHRIN-BINDING (BY SIMILARITY).  
 FT DISULFID 291 341  
 FT BY SIMILARITY.  
 FT DISULFID 300 324  
 FT BY SIMILARITY.  
 FT DISULFID 316 337  
 FT BY SIMILARITY.  
 FT CARBOHYD 542 542  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 571 571  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPPLIC 289 289  
 FT E -> V (IN ISOFORM APP(695)).  
 FT VARSPPLIC 290 364  
 FT MISSING (IN ISOFORM APP(695)).  
 FT VARSPPLIC 346 380  
 FT MISSING (IN ISOFORM APP(751)).  
 FT SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;  
 SQ

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Query Match      80.0%; Score 44; DB 1; Length 770;
Best Local Similarity 88.9%; Pred. No. 0.43;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HQKLVFFAQ 10
Db 685 HQKLVFFAE 693

RESULT 10
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07648; CAA30488.1; -
DR EMBL; X14086; CAA32229.1; -
DR PIR; S00550; S00550.
DR PIR; S03607; S03607.
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT HOMOLOG.
FT DOMAIN 18 699
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 700 723
FT POTENTIAL.
FT DOMAIN 724 770
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 673 715
FT EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT DOMAIN 287 345
FT BPTI/KUNITZ INHIBITOR.
FT SITE 759 762
FT CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 291 341
FT BY SIMILARITY.
FT DISULFID 300 324
FT BY SIMILARITY.
FT DISULFID 316 337
FT BY SIMILARITY.
FT CARBOHYD 542 542
FT N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 571 571
FT N-LINKED (GLCNAC... ) (POTENTIAL).
FT VARSPLIC 289 289
FT E -> V (IN ISOFORM APP(695)).
FT VARSPLIC 290 364
FT MISSING (IN ISOFORM APP(695)).
SQ SEQUENCE 770 AA; 86704 MW; C26C9D68B2D929A7 CRC64;

Query Match      80.0%; Score 44; DB 1; Length 770;
Best Local Similarity 88.9%; Pred. No. 0.43;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HQKLVFFAQ 10
Db 685 HQKLVFFAE 693

RESULT 11
G6PI_ECOLI
ID G6PI_ECOLI STANDARD; PRT; 549 AA.
AC P11537;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) [Phosphohexose isomerase] (PHI).
GN PGI OR B4025 OR Z5623 OR ECS5008.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JM101.
RX MEDLINE=89364675; PubMed=2549364;
RA Froman B.E., Tait R.C., Gottlieb L.D.;
RT "Isolation and characterization of the phosphoglucose isomerase gene
RT from Escherichia coli.";
RL Mol. Gen. Genet. 217:126-131(1989).
RN [2]
RP SEQUENCE FROM N.A., AND PHYLOGENETIC STUDY.
RC STRAIN=XLI BLUE 2;
RX MEDLINE=92277670; PubMed=1593646;
RA Smith M.W., Doolittle R.F.;
RT "Anomalous phylogeny involving the enzyme glucose-6-phosphate
RT isomerase.";
RL J. Mol. Evol. 34:544-545(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
```

```

RT region from 89.2 to 92.8 minutes.";
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [4]
RC SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RT Nature 409:529-533(2001).
RN [5]
RC SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11256796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
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CC -----
EMBL; X15196; CAA33268.1; -.
DR EMBL; U00006; AAC43119.1; -.
DR EMBL; AE000476; AAC76995.1; -.
DR EMBL; AE005635; AAG59224.1; -.
DR EMBL; AP002568; BAB38431.1; -.
DR PIR; JS0142; NUC.
DR EcoGene; EG10702; pgi.
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; PGI; 1.
DR PRINTS; PR00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT ACT_SITE 386 386 BY SIMILARITY.
FT ACT_SITE 514 514 BY SIMILARITY.
FT CONFLICT 317 317 L->V (IN REF. 1 AND 2).
SQ SEQUENCE 549 AA; 61529 MW; 74AEDB70A068A01 CRC64;

Query Match 74.5%; Score 41; DB 1; Length 549;
Best Local Similarity 75.0%; Pred. No. 1.2;
Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 HHQKLV--FFAQ 10
Db 416 HHQKLSNFFAQ 427
|||||: ||||
|:|:|:|:|

RESULT 12
G6PI_VIBCH
ID G6PI_VIBCH STANDARD; PRT; 550 AA.
AC Q9KUY4;
DT 01-MAR-2002 (Rel. 41, Created)

region from 89.2 to 92.8 minutes.";
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [4]
RC SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RT Nature 409:529-533(2001).
RN [5]
RC SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11256796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
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CC -----
EMBL; X15196; CAA33268.1; -.
DR EMBL; U00006; AAC43119.1; -.
DR EMBL; AE000476; AAC76995.1; -.
DR EMBL; AE005635; AAG59224.1; -.
DR EMBL; AP002568; BAB38431.1; -.
DR PIR; JS0142; NUC.
DR EcoGene; EG10702; pgi.
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; PGI; 1.
DR PRINTS; PR00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT ACT_SITE 386 386 BY SIMILARITY.
FT ACT_SITE 514 514 BY SIMILARITY.
FT CONFLICT 317 317 L->V (IN REF. 1 AND 2).
SQ SEQUENCE 549 AA; 61529 MW; 74AEDB70A068A01 CRC64;

Query Match 74.5%; Score 41; DB 1; Length 549;
Best Local Similarity 75.0%; Pred. No. 1.2;
Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 HHQKLV--FFAQ 10
Db 416 HHQKLSNFFAQ 427
|||||: ||||
|:|:|:|:|

RESULT 13
MALQ_HAEIN
ID MALQ_HAEIN STANDARD; PRT; 699 AA.
AC P45176;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase)
DE (Disproportionating enzyme) (D-enzyme).
CN MALQ OR H11356
OS Haemophilus influenzae.
CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC Haemophilus.
CC NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.

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DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR VC0374.
OS Vibrio cholerae.
CC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
CC NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
CC -1- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE = FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
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CC -----
EMBL; AE004125; AAF93547.1; -.
DR TIGR; VC0374; -.
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; PGI; 1.
DR PRINTS; PR00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT ACT_SITE 387 387 BY SIMILARITY.
FT ACT_SITE 515 515 BY SIMILARITY.
SQ SEQUENCE 550 AA; 60690 MW; 5E38B0421C3A1B16 CRC64;

Query Match 74.5%; Score 41; DB 1; Length 550;
Best Local Similarity 75.0%; Pred. No. 1.2;
Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 HHQKLV--FFAQ 10
Db 417 HHQKLSNFFAQ 428
|||||: ||||
|:|:|:|:|

RESULT 13
MALQ_HAEIN
ID MALQ_HAEIN STANDARD; PRT; 699 AA.
AC P45176;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase)
DE (Disproportionating enzyme) (D-enzyme).
CN MALQ OR H11356
OS Haemophilus influenzae.
CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC Haemophilus.
CC NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.

```

```
RC STRAIN-RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7342800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA McLavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -|- CATALYTIC ACTIVITY: Transfers a segment of a (1,4)-alpha-D-glucan
CC to a new 4-position in an acceptor, which may be glucose or (1,4)-
CC alpha-D-glucan.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE DISPROPORTIONATING ENZYME FAMILY.
CC
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CC
CC -----
CC EMBL: U32815; AAC23003.1; -.
CC TIGR: H11356; -.
CC InterPro: IPR003385; 4A-glucanotrans.
CC Pfam: PF02446; 4A-glucanotrans; 1.
CC Transferrase; Glycosyltransferase; Carbohydrate metabolism;
KW Complete proteome.
SQ SEQUENCE 699 AA; 80251 MW; 80D6E1D51EC2E1E9 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 699;
Best Local Similarity 66.7%; Pred. No. 3.8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
||:|:||||
DB 349 HHEKIQFFA 357

RESULT 14
G6PI_BUCAI
ID G6PI_BUCAI STANDARD; PRT; 549 AA.
AC P57636;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
DE PGI OR BU573.
GN Shigella aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TOKYO 1998;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -|- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -|- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: AP001119; BAB13263.1; -.
CC InterPro: IPR001672; G6P_Isomerase.
CC Pfam: PF0342; PGI; 1.
CC PRINTS: PR00662; G6PISOMERASE.
CC PROSITE: PS00765; P_GLUCOSE_ISOMERASE.1; 1.
CC PROSITE: PS00174; P_GLUCOSE_ISOMERASE.2; 1.
KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT ACT_SITE 386 386 BY SIMILARITY.
FT ACT_SITE 514 514 BY SIMILARITY.
SQ SEQUENCE 549 AA; 63435 MW; 8DF547CE08382244 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 549;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 1 HHOKLV-FFAQ 10
||:|:||||
DB 416 HHMKLISNFFAQ 427

RESULT 15
G6PI_PASMU
ID G6PI_PASMU STANDARD; PRT; 549 AA.
AC Q9CNL2;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
DE PGI OR PM0416.
GN Pasteurella multocida.
OS Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PM70;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -|- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE = FRUCTOSE 6-PHOSPHATE.
CC -|- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: AE006077; AAK02500.1; -.
CC InterPro: IPR001672; G6P_Isomerase.
CC Pfam: PF0342; PGI; 1.
CC PRINTS: PR00662; G6PISOMERASE.
CC PROSITE: PS00765; P_GLUCOSE_ISOMERASE.1; 1.
CC PROSITE: PS00174; P_GLUCOSE_ISOMERASE.2; 1.
KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT ACT_SITE 387 387 BY SIMILARITY.
FT ACT_SITE 515 515 BY SIMILARITY.
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SQ SEQUENCE 549 AA; 61437 MW; E6E4856927B93283 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 549;  
Best Local Similarity 66.7%; Pred. No. 4.7;  
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

Qy 1 HHQKLV--FFAQ 10  
||:|:|:|  
Db 417 HHEKLLSNFFAQ 428

Search completed: July 18, 2002, 10:17:39  
Job time: 66 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 18, 2002, 10:16:13 ; Search time 25.17 Seconds  
(without alignments)  
68.731 Million cell updates/sec

Title: US-09-724-842-27  
Perfect score: 55  
Sequence: 1 HHQKLVFFAQ 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp-unclassified:\*  
15: sp-rvrius:\*  
16: sp-bacteriap:\*  
17: sp-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	94.5	28	4 Q9UCD1	Q9ucd1 homo sapien
2	52	94.5	30	4 Q9UCA9	Q9uca9 homo sapien
3	52	94.5	33	4 Q9UC33	Q9uc33 homo sapien
4	52	94.5	82	4 P78438	P78438 homo sapien
5	52	94.5	82	4 Q16014	Q16014 homo sapien
6	52	94.5	82	4 Q16019	Q16019 homo sapien
7	52	94.5	82	4 Q16020	Q16020 homo sapien
8	52	94.5	97	4 Q13778	Q13778 homo sapien
9	52	94.5	534	13 O93296	O93296 gallus gall
10	52	94.5	569	13 Q9PVL1	Q9pvl1 gallus gall
11	52	94.5	693	13 Q98SG0	Q98sg0 xenopus lae
12	52	94.5	695	6 Q95KN7	Q95kn7 macaca fasc
13	52	94.5	695	11 Q60496	Q60496 cavia sp. p
14	52	94.5	695	13 Q9PGJ8	Q9pgj8 gallus gall
15	52	94.5	747	13 Q91963	Q91963 xenopus. ap
16	52	94.5	751	13 Q9PGJ7	Q9pgj7 gallus gall

17	52	94.5	770	6 Q9TUI0	Q9tui0 sus scrofa
18	52	94.5	780	13 Q93683	Q93683 tetraodon f
19	50	90.9	695	13 Q98SF9	Q98sf9 xenopus lae
20	46	83.6	612	13 Q919E7	Q919e7 brachydanio
21	46	83.6	699	13 Q57394	Q57394 narke japon
22	46	83.6	738	13 Q90W28	Q90w28 brachydanio
23	44	80.0	79	11 Q35463	Q35463 cricetus
24	44	80.0	607	11 Q99K32	Q99k32 mus musculu
25	44	80.0	695	11 P97487	P97487 mus musculu
26	44	80.0	737	13 Q93279	Q93279 fugu rubrip
27	41	74.5	326	2 Q9K376	Q9k376 escherichia
28	41	74.5	326	2 Q9K328	Q9k328 escherichia
29	41	74.5	326	2 Q9K273	Q9k273 escherichia
30	41	74.5	326	2 Q9K2R7	Q9k2r7 escherichia
31	41	74.5	326	2 Q9K2Q3	Q9k2q3 escherichia
32	41	74.5	326	2 Q9KH87	Q9kh87 escherichia
33	41	74.5	326	2 Q9KH85	Q9kh85 escherichia
34	41	74.5	326	2 Q9KH84	Q9kh84 escherichia
35	40	72.7	19	4 Q9UC8	Q9uc8 homo sapien
36	40	72.7	191	10 Q9SN52	Q9sn52 arabidopsis
37	40	72.7	584	5 Q9UOM8	Q9uom8 plasmodium
38	38	69.1	272	16 P96882	P96882 mycobacteri
39	37	67.3	326	2 Q9KH86	Q9kh86 escherichia
40	37	67.3	354	2 Q93CU7	Q93cu7 shigella bo
41	37	67.3	626	16 Q9KI85	Q9ki85 neisseria m
42	37	67.3	635	16 Q9JSP1	Q9jspl neisseria m
43	37	67.3	1035	2 Q93E19	Q93e19 acinetobact
44	36	65.5	103	6 Q9XST6	Q9xst6 canis famil
45	36	65.5	152	11 Q9CUI7	Q9cuy7 mus musculu

ALIGNMENTS

RESULT 1  
Q9UCD1 ID Q9UCD1 PRELIMINARY; PRT; 28 AA.  
AC Q9UCD1;  
DT 01-MAY-2000 (T:EMBLrel. 13, Created)  
DT 01-MAY-2000 (T:EMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (T:EMBLrel. 16, Last annotation update)  
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=94045635; PubMed=8229004;  
RA Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;  
RT "Characterization of beta-amyloid peptide from human cerebrospinal fluid.";  
RL J. Neurochem. 51:1965-1968(1993).  
DR HSSP; P05067; IAMB.  
SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;

Query Match 94.5%; Score 52; DB 4; Length 28;  
Best Local Similarity 90.0%; Pred. No. 0.0015;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Caps 0;

QY 1 HHQKLVFFAQ 10  
| | | | | | | | | |  
Db 13 HHQKLVFFAE 22

RESULT 2  
Q9UCA9 ID Q9UCA9 PRELIMINARY; PRT; 30 AA.  
AC Q9UCA9;  
DT 01-MAY-2000 (T:EMBLrel. 13, Created)  
DT 01-MAY-2000 (T:EMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (T:EMBLrel. 16, Last annotation update)

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DE BETA-AMYLOID PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94153015; PubMed=8109908;
RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT "The amino acid sequence of neuritic plaque amyloid from a familial
  Alzheimer's disease patient.";
RL Ann. Neurol. 35:245-246(1994).
DR HSSP; P05067; 1BA4.
SQ SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;

Query Match          94.5%; Score 52; DB 4; Length 30;
Best Local Similarity 90.0%; Pred. No. 0.0016;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFFAQ 10
Db 13 HHQKLVFFFAE 22

RESULT 3
Q9UC33
ID Q9UC33 PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
  Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
  biological fluids.";
RL Nature 359:325-327(1992).
DR HSSP; P05067; 1BA4.
SQ SEQUENCE 33 AA; 3674 MW; B1DFE2F4167ABD0 CRC64;

Query Match          94.5%; Score 52; DB 4; Length 33;
Best Local Similarity 90.0%; Pred. No. 0.0018;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFFAQ 10
Db 13 HHQKLVFFFAE 22

RESULT 4
P78438
ID P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
  Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
  similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
  Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
  linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,
  Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
  kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -.
DR EMBL; M29269; AAA51768.1; JOINED.
DR EMBL; M15532; AAA51564.1; -.
DR EMBL; S45136; AAB23646.1; -.
DR HSSP; P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match          94.5%; Score 52; DB 4; Length 82;
Best Local Similarity 90.0%; Pred. No. 0.0045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFFAQ 10
Db 29 HHQKLVFFFAE 38

RESULT 5
Q16014
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
  mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSSP; P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match          94.5%; Score 52; DB 4; Length 82;
Best Local Similarity 90.0%; Pred. No. 0.0045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFFAQ 10
Db 30 HHQKLVFFFAE 39

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RESULT 6
ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019:
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
OS BETA APP.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -.
DR HSSP; P05067; 1BA4.
DR NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 94.5%; Score 52; DB 4; Length 82;
Best Local Similarity 90.0%; Pred. No. 0.0045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVEFFAQ 10
   | | | | | | | | | |
Db 30 HHQKLVEFFAE 39

RESULT 7
ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020:
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
OS BETA APP.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -.
DR HSSP; P05067; 1BA4.
DR NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 94.5%; Score 52; DB 4; Length 82;
Best Local Similarity 90.0%; Pred. No. 0.0045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVEFFAQ 10
   | | | | | | | | | |
Db 30 HHQKLVEFFAE 39

RESULT 8
ID Q13778 PRELIMINARY; PRT; 97 AA.
AC Q13778:
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

Query Match 94.5%; Score 52; DB 4; Length 97;
Best Local Similarity 90.0%; Pred. No. 0.0053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVEFFAQ 10
   | | | | | | | | | |
Db 11 HHQKLVEFFAE 20

RESULT 9
ID O93296 PRELIMINARY; PRT; 534 AA.
AC O93296:
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR NON_TER 1
FT NON_TER 534
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 94.5%; Score 52; DB 13; Length 534;
Best Local Similarity 90.0%; Pred. No. 0.031;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVEFFAQ 10

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Db 448 HHQKLVEFAE 457  
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## RESULT 10

Q9PVL1 Q9PVL1 PRELIMINARY; PRT; 569 AA.  
AC Q9PVL1  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE AMYLOID PROTEIN (FRAGMENT).  
GN APP.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;  
RT "What the evolution of the amyloid protein precursor supergene family  
tells us about its function."  
RL Neurochem. Int. 0:0-0(2000).  
DR EMBL; AF030341; AAF12698.1; -.  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001868; A4\_APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
FT NON\_TER 1  
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 94.5%; Score 52; DB 13; Length 569;  
Best Local Similarity 90.0%; Pred. No. 0.033;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVEFAQ 10  
|||||

## RESULT 11

Q98SG0 Q98SG0 PRELIMINARY; PRT; 693 AA.  
AC Q98SG0  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE BETA-AMYLOID PRECURSOR PROTEIN A.  
GN APP.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA van den Hurk W.H.;  
RL Thesis (2001), Department of Biological Sciences,  
RL University of Nijmegen, Nijmegen, Netherlands.  
DR EMBL; AJ298150; CAC37193.1; -.  
DR HSSP; P05067; 1H23.  
DR InterPro; IPR001868; A4\_APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.

KW Signal. 1 18 POTENTIAL.  
FT SIGNAL 693 AA; 78568 MW; CAF1DF655CIAB653 CRC64;  
SQ SEQUENCE

Query Match 94.5%; Score 52; DB 13; Length 693;  
Best Local Similarity 90.0%; Pred. No. 0.04;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVEFAQ 10  
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Db 607 HHQKLVEFAE 616  
|||||

## RESULT 12

Q95KN7 Q95KN7 PRELIMINARY; PRT; 695 AA.  
AC Q95KN7  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE AMYLOID B-PROTEIN PRECURSOR.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-CEREBELLUM;  
RX MEDLINE-91273117; PubMed-1905108;  
RA Podlinsky M.B., Tolan D.R., Seikoe D.J.;  
RT "Homology of the amyloid beta protein precursor in monkey and human  
supports a primate model for beta amyloidosis in Alzheimer's  
disease."  
RL Am. J. Pathol. 138:1423-1435(1991).  
DR EMBL; M58727; AAA36829.1; -. POTENTIAL.  
FT SIGNAL 1 17  
FT CHAIN 597 636  
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 94.5%; Score 52; DB 6; Length 695;  
Best Local Similarity 90.0%; Pred. No. 0.04;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVEFAQ 10  
|||||

Db 609 HHQKLVEFAE 618  
|||||

## RESULT 13

Q60496 Q60496 PRELIMINARY; PRT; 695 AA.  
AC Q60496  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.  
OS Cavia sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10143;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE-97236426; PubMed-9116031;  
RA Beck M., Mueller D., Bigl V.;  
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and  
alternative splicing."  
RL Biochim. Biophys. Acta 1351:17-21(1997).  
DR EMBL; X97631; CAA66230.1; -.  
DR HSSP; P05067; 1BA4.

DR InterPro: IPR001868; A4\_APP.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRA; 1.  
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 94.5%; Score 52; DB 11; Length 695;  
Best Local Similarity 90.0%; Pred. No. 0.04;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
|||||  
DB 609 HHQKLVFFAE 618

RESULT 14  
Q9DGJ8 PRELIMINARY; PRT; 695 AA.  
AC Q9DGJ8;  
DT 01-WAR-2001 (TREMBLrel. 16, Created)  
DT 01-WAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sarasa M., Rodolase A., Sorribas V.;  
RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF289218; AAG00593.1; -;  
DR HSSP: P05067; 1BA4.  
DR InterPro: IPR001868; A4\_APP.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 94.5%; Score 52; DB 13; Length 695;  
Best Local Similarity 90.0%; Pred. No. 0.04;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
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DB 609 HHQKLVFFAE 618

RESULT 15  
Q91963 PRELIMINARY; PRT; 747 AA.  
AC Q91963;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE APP747.  
GN APP747.  
OS Xenopus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae.  
OX NCBI\_TaxID=8353;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93129227; PubMed=1282805;

RA Okado H., Okamoto H.;  
RT "A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression";  
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).  
DR EMBL: S52417; AAB24853.1; -;  
DR HSSP: P05067; 1HZ3.  
DR InterPro: IPR001868; A4\_APP.  
DR InterPro: IPR002223; Kunitz\_BPTI.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR Pfam: PF00014; Kunitz\_BPTI; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR PRINTS: PR00759; BASICPTASE.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR SMART: SM00131; KU; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRA; 1.  
DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE: PS0279; BPTI\_KUNITZ\_2; 1.  
KW Serine protease inhibitor.  
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 94.5%; Score 52; DB 13; Length 747;  
Best Local Similarity 90.0%; Pred. No. 0.044;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
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DB 661 HHQKLVFFAE 670

Search completed: July 18, 2002, 10:17:22  
Job time: 69 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 18, 2002, 10:13:48 ; Search time 13.06 Seconds  
(without alignments)  
18.703 Million cell updates/sec

Title: US-09-724-842-27  
Perfect score: 55  
Sequence: 1 HHOKLVFFAQ 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	28	4 US-09-388-890-12	Sequence 12, Appl
2	55	100.0	40	1 US-08-304-585-8	Sequence 8, Appl
3	55	100.0	63	1 US-08-462-859A-3	Sequence 3, Appl
4	55	100.0	63	1 US-08-123-659A-3	Sequence 3, Appl
5	55	100.0	63	1 US-08-464-247A-3	Sequence 3, Appl
6	55	100.0	63	1 US-08-464-248A-3	Sequence 3, Appl
7	55	100.0	99	3 US-08-339-708A-6	Sequence 6, Appl
8	52	94.5	15	2 US-08-612-785B-37	Sequence 37, Appl
9	52	94.5	17	4 US-09-264-709A-2	Sequence 2, Appl
10	52	94.5	26	1 US-08-304-585-7	Sequence 7, Appl
11	52	94.5	28	1 US-08-346-849-4	Sequence 4, Appl
12	52	94.5	28	1 US-08-302-808-7	Sequence 7, Appl
13	52	94.5	28	2 US-08-609-090-2	Sequence 2, Appl
14	52	94.5	28	2 US-08-986-948-7	Sequence 7, Appl
15	52	94.5	28	2 US-08-293-284A-4	Sequence 4, Appl
16	52	94.5	28	2 US-08-461-216-2	Sequence 2, Appl
17	52	94.5	28	4 US-09-388-890-2	Sequence 2, Appl
18	52	94.5	28	4 US-09-388-890-3	Sequence 3, Appl
19	52	94.5	28	4 US-09-388-890-4	Sequence 4, Appl
20	52	94.5	28	4 US-09-388-890-5	Sequence 5, Appl
21	52	94.5	28	4 US-09-388-890-6	Sequence 6, Appl
22	52	94.5	28	4 US-09-388-890-7	Sequence 7, Appl
23	52	94.5	28	4 US-09-388-890-8	Sequence 8, Appl
24	52	94.5	28	4 US-09-388-890-13	Sequence 13, Appl
25	52	94.5	28	4 US-09-388-890-14	Sequence 14, Appl
26	52	94.5	28	4 US-09-264-709A-1	Sequence 1, Appl
27	52	94.5	28	4 US-08-723-661B-2	Sequence 2, Appl

28	52	94.5	30	2 US-08-609-090-3	Sequence 3, Appl
29	52	94.5	33	2 US-08-609-090-4	Sequence 4, Appl
30	52	94.5	35	1 US-08-304-585-6	Sequence 6, Appl
31	52	94.5	35	2 US-08-612-785B-36	Sequence 36, Appl
32	52	94.5	35	2 US-08-612-785B-38	Sequence 38, Appl
33	52	94.5	35	2 US-08-612-785B-40	Sequence 40, Appl
34	52	94.5	36	2 US-08-609-090-6	Sequence 6, Appl
35	52	94.5	38	1 US-08-302-808-1	Sequence 1, Appl
36	52	94.5	38	2 US-07-737-371E-68	Sequence 68, Appl
37	52	94.5	38	2 US-08-986-948-1	Sequence 1, Appl
38	52	94.5	39	1 US-08-304-585-5	Sequence 5, Appl
39	52	94.5	39	1 US-08-302-808-2	Sequence 2, Appl
40	52	94.5	39	2 US-08-609-090-7	Sequence 7, Appl
41	52	94.5	39	2 US-08-682-245A-1	Sequence 1, Appl
42	52	94.5	39	2 US-08-986-948-2	Sequence 2, Appl
43	52	94.5	40	1 US-07-744-767A-1	Sequence 1, Appl
44	52	94.5	40	1 US-08-235-400-2	Sequence 2, Appl
45	52	94.5	40	1 US-08-476-464A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-388-890-12  
; Sequence 12, Application US/09388890  
; Patent No. 6136548  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, STEPHEN  
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT  
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWREY & SIMON  
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: US  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/388,890  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/686,959  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: AUERBACH, JEFFREY I.  
; REGISTRATION NUMBER: 32,680  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 383-7451  
; TELEFAX: (202) 383-6610  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: YES  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: HOMO SAPIENS  
; IMMEDIATE SOURCE:  
; CLONE: E22Q B(1-28) peptide of amyloid B protein  
; US-09-388-890-12

Query Match 100.0%; Score 55; DB 4; Length 28;

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Best Local Similarity 100.0%; Pred. No. 0.00026; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 1 HHQKLVFFAQ 10
Db 13 HHQKLVFFAQ 22

RESULT 2
US-08-304-585-8
; Sequence 8, Application US/08304585
; Patent No. 5721106
; GENERAL INFORMATION:
; APPLICANT: Magglio, John E.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P. A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-304-585-8

Query Match 100.0%; Score 55; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
Db 13 HHQKLVFFAQ 22

RESULT 3
US-08-462-859A-3
; Sequence 3, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5652092a1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
```

```
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-3

Query Match 100.0%; Score 55; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
Db 22 HHQKLVFFAQ 31

RESULT 4
US-08-123-659A-3
; Sequence 3, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; TITLE OF INVENTION: No. 5656477a1 Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
```

TELEFAX: (518)475-0619  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 63 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-123-659A-3

Query Match 100.0%; Score 55; DB 1; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0.00061;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFFAQ 10  
 |||||  
 DB 22 HHOKLVFFFAQ 31

RESULT 5

US-08-464-247A-3  
 Sequence 3, Application US/08464247A  
 Patent No. 5693478

GENERAL INFORMATION:  
 APPLICANT: Jacobsen, J. S.  
 APPLICANT: Vitek, M. P.  
 TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of  
 TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
 TITLE OF INVENTION: of B-Amyloid Peptide  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: American Cyanamid Company  
 STREET: One Campus Drive  
 CITY: Parsippany  
 STATE: New Jersey  
 COUNTRY: United States  
 ZIP: 07054

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464,247A  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barnhard, Elizabeth M.  
 REGISTRATION NUMBER: 31,088  
 REFERENCE/DOCKET NUMBER: 31,844-03  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-683-2158  
 TELEFAX: 201-683-4117

INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 63 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-464-247A-3

Query Match 100.0%; Score 55; DB 1; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0.00061;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFFAQ 10  
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 DB 22 HHOKLVFFFAQ 31

RESULT 6

US-08-464-248A-3  
 Sequence 3, Application US/08464248A  
 Patent No. 5703209

GENERAL INFORMATION:  
 APPLICANT: Jacobsen, J. S.  
 APPLICANT: Vitek, M. P.  
 TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
 TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
 TITLE OF INVENTION: of B-Amyloid Peptide  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: American Cyanamid Company  
 STREET: One Cyanamid Plaza  
 CITY: Wayne  
 STATE: New Jersey  
 COUNTRY: United States  
 ZIP: 07470-8426

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464,248A  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barnhard, Elizabeth M.  
 REGISTRATION NUMBER: 31,088  
 REFERENCE/DOCKET NUMBER: 31,844-02  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201)831-3246  
 TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 63 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-464-248A-3

Query Match 100.0%; Score 55; DB 1; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0.00061;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFFAQ 10  
 |||||  
 DB 22 HHOKLVFFFAQ 31

RESULT 7

US-08-339-708A-6  
 Sequence 6, Application US/08339708A  
 Patent No. 6037521

GENERAL INFORMATION:  
 APPLICANT: Sato, Masahiro  
 APPLICANT: Takashi, Kobayashi  
 APPLICANT: Tada, No. 6037521hiro  
 APPLICANT: Shoji, Mikio  
 APPLICANT: Kawarabayashi, Takeshi  
 TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S  
 TITLE OF INVENTION: DISEASE  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/339,708A  
APPLICATION NUMBER: US/08/339,708A  
FILING DATE: 14-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 306026/93  
FILING DATE: 12-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: SANDERCOCK, COLIN G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 026083/0159  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-339-708A-6

Query Match 100.0%; Score 55; DB 3; Length 99;  
Best Local Similarity 100.0%; Pred. No. 0.00098;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10  
Db 13 HHQKLVFFAQ 22

RESULT 8  
US-08-612-785B-37  
Sequence 37, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: AD peptides that Modulate b-Amyloid  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-612-785B-37

Query Match 94.5%; Score 52; DB 2; Length 15;  
Best Local Similarity 90.0%; Pred. No. 0.00051;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10  
Db 3 HHQKLVFFAE 12

RESULT 9  
US-09-264-709A-2  
Sequence 2, Application US/09264709A  
Patent No. 6320024  
GENERAL INFORMATION:  
APPLICANT: Roberts, Eugene  
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and  
FILE OF INVENTION: Improve the Quality of Life  
FILE REFERENCE: 2124-310  
CURRENT APPLICATION NUMBER: US/09/264,709A  
CURRENT FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: 08/797,782  
PRIOR FILING DATE: 1997-02-07  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-264-709A-2

Query Match 94.5%; Score 52; DB 4; Length 17;  
Best Local Similarity 90.0%; Pred. No. 0.00058;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10  
Db 2 HHQKLVFFAE 11

RESULT 10  
US-08-304-585-7  
Sequence 7, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Maggio, John E.  
APPLICANT: Mantyh, Patrick W.  
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 581415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk



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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-304-585-7

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Query Match          94.5%; Score 52; DB 1; Length 26;
Best Local Similarity 90.0%; Pred. No. 0.0009;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HHOKLVFFAQ 10
Db 4 HHOKLVFFAE 13

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RESULT 11
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-346-849-4

Query Match          94.5%; Score 52; DB 1; Length 28;
Best Local Similarity 90.0%; Pred. No. 0.00098;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10
Db 13 HHOKLVFFAE 22

RESULT 12
US-08-302-808-7
; Sequence 7, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal

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ORIGINAL SOURCE:  
US-08-302-808-7

Query Match 94.5%; Score 52; DB 1; Length 28;  
Best Local Similarity 90.0%; Pred. No. 0.00098;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLFFFAQ 10  
Db 13 HHQKLFFFAE 22

## RESULT 13

US-08-609-090-2

; Sequence 2, Application US/08609090

; Patent No. 5840838

; GENERAL INFORMATION:

; APPLICANT: HENSLEY, Kenneth

; APPLICANT: BUTTERFIELD, D. A.

; APPLICANT: CARNEY, John M.

; APPLICANT: AKSENOV, Michael

; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LOWE PRICE LEBLANC & BECKER

; STREET: 99 Canal Center Plaza, Suite 300

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/08/609,090

; APPLICATION NUMBER: US/08/609,090

; FILING DATE: 29-FEB-1996

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Kraus, Eric J.

; REGISTRATION NUMBER: 36,190

; REFERENCE/DOCKET NUMBER: 434-059

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-684-1111

; TELEFAX: 703-684-1124

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-609-090-2

Query Match 94.5%; Score 52; DB 2; Length 28;  
Best Local Similarity 90.0%; Pred. No. 0.00098;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLFFFAQ 10  
Db 13 HHQKLFFFAE 22

## RESULT 14

US-08-986-948-7

; Sequence 7, Application US/08986948

; Patent No. 5955317

; GENERAL INFORMATION:

; APPLICANT: SUZUKI, No. 5955317uhiro

; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA: US/08/986,948  
; APPLICATION NUMBER: US/08/986,948  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/302,808  
; FILING DATE: 15-SEP-1994  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; US-08-986-948-7

Query Match 94.5%; Score 52; DB 2; Length 28;  
Best Local Similarity 90.0%; Pred. No. 0.00098;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLFFFAQ 10  
Db 13 HHQKLFFFAE 22

## RESULT 15

US-08-293-284A-4

; Sequence 4, Application US/08293284A

; Patent No. 5955343

; GENERAL INFORMATION:

; APPLICANT: Holmes, Todd

; APPLICANT: Zhang, Shuguang

; APPLICANT: Rich, Alexander

```

; APPLICANT: DIPERSIO, C. Michael
; APPLICANT: Lockshin, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,284A
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOK, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-284A-4

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Query Match          94.5%; Score 52; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 0.00098;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HHOKLVFFAQ 10
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Db 13 HHOKLVFFAE 22

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Job time: 161 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:16:39 ; Search time 29.95 Seconds  
(without alignments)  
37.086 Million cell updates/sec

Title: US-09-724-842-27

Perfect score: 10

Sequence: 1 HHQKLVFFAQ 10

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Gapop 60.0 , Capext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	10	100.0	35	22	AA891830
6	10	100.0	40	19	AAW47232
7	10	100.0	53	15	AA855697
8	10	100.0	63	18	AAW26511
9	10	100.0	63	18	AAW26391
10	10	100.0	63	19	AAW44746
11	10	100.0	63	19	AAW42975

12	10	100.0	99	16	AA874695	Beta-amyloid precu
13	9	90.0	9	22	AA848493	Antifibrillogenic
14	9	90.0	10	22	AA846224	Human APP derived
15	9	90.0	10	22	AA846225	Human APP derived
16	9	90.0	15	20	AA893358	Beta-amyloid pept1
17	9	90.0	17	15	AA854703	Beta-amyloid fragm
18	9	90.0	17	22	AA891774	Amyloid beta-prote
19	9	90.0	17	22	AA891807	Amyloid beta-prote
20	9	90.0	17	22	AA848346	Beta-amyloid anti
21	9	90.0	18	21	AA810963	Beta-amyloid precu
22	9	90.0	19	18	AAW18882	ADANS-beta-amyloi
23	9	90.0	19	18	AAW18881	Trp-Beta-amyloid p
24	9	90.0	19	22	AA846201	Human APP A-beta 1
25	9	90.0	19	22	AA849097	Human amyloid beta
26	9	90.0	21	20	AA830941	Human secretase SE
27	9	90.0	24	15	AA852569	Alzheimer's diseas
28	9	90.0	26	19	AAW47229	Beta-amyloid pept1
29	9	90.0	26	20	AA833408	Human amyloidogeni
30	9	90.0	27	20	AA833409	Human amyloidogeni
31	9	90.0	28	8	AA870594	Sequence of Alzhei
32	9	90.0	28	10	AA890381	Synthetic A4 amylo
33	9	90.0	28	15	AA854702	Beta-amyloid fragm
34	9	90.0	28	15	AA860368	Beta-amyloid (1-28
35	9	90.0	28	15	AA864170	A4-O(1-28) a parti
36	9	90.0	28	16	AA864171	A4-P(1-28) a parti
37	9	90.0	28	16	AA864172	A4-B(1-28) a parti
38	9	90.0	28	16	AA864173	Generic beta amylo
39	9	90.0	28	17	AAW01413	Beta/A4-amyloid pe
40	9	90.0	28	20	AA839805	Beta-amyloid prote
41	9	90.0	28	20	AA81467	Synthetic amyloid
42	9	90.0	28	22	AA891783	Amyloid beta-prote
43	9	90.0	28	22	AA891789	Amyloid beta-prote
44	9	90.0	28	22	AA891800	Amyloid beta-prote
45	9	90.0	28	22	AA891816	Amyloid beta-prote

#### ALIGNMENTS

RESULT	1
AA82641	
ID	AA82641 standard; Peptide; 10 AA.
XX	
AC	AA82641;
XX	
DT	02-OCT-2001 (first entry)
XX	
DE	All-D peptide used in Alzheimer's disease vaccine.
XX	
KW	Alzheimer's disease; amyloidosis; amyloid-related disease;
KW	vaccine; therapy; antigen.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Misc-difference 1..10
XX	/note= "all D-form residues"
XX	
PN	WO200139796-A2.
XX	
PD	07-JUN-2001.
XX	
PF	29-NOV-2000; 2000WO-CA01413.
XX	
PR	29-NOV-1999; 99US-0168594.
XX	
PR	28-NOV-2000; 2000US-0724842.
XX	
PA	(NEUR-) NEUROCHEM INC.
XX	
PI	Chalfour R, Hebert L, Kong X, Gervais F;
XX	
DR	WPI; 2001-441458/47.
XX	

PT Preventing/treating amyloid-related disease, especially Alzheimer's  
 PT disease, comprises administering antigenic all-D peptide, e.g. as  
 PT vaccine, which elicits production of antibodies to prevent  
 PT fibrillogenesis and associated cellular toxicity -

XX Disclosure; Page 11; 31pp; English.

CC The present sequence is that of an all-D peptide suitable for  
 CC use in preparing vaccines for preventing or treating Alzheimer's  
 CC disease and other amyloid related disorders in humans. It is based  
 CC on a portion of amyloid-beta peptide (see AAB82622), and may be  
 CC modified by removing or inserting 1 or more amino acid residues, or  
 CC by substituting 1 or more amino acid residues with other amino acid  
 CC residues or non-amino acid fragments. Vaccines of the invention  
 CC are produced using 'non-self' peptides synthesised from the  
 CC unnatural D-configuration amino acids to avoid the drawbacks of  
 CC 'self' proteins. The all-D peptides need not be aggregated to be  
 CC operative or immunogenic. They preferably interact with at  
 CC least 1 region of an amyloid protein, e.g. the beta-sheet region  
 CC or GAG-binding site region, the amyloid-beta peptide, or their  
 CC immunogenic fragments, protein conjugates, immunogenic derivative  
 CC peptides and immunogenic peptidomimetics. Examples include all-D  
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,  
 CC 10-15, 16-21 and 36-42 of the amyloid-beta peptide and the all-D  
 CC derivative peptides given in AAB82623-64. The vaccine elicits a  
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and  
 CC associated cellular toxicity. The amyloid related diseases may be  
 CC localised amyloidosis, e.g. diabetes type II, neurodegenerative  
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob  
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein  
 CC related disorders, or systemic amyloidosis associated with chronic  
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.  
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and  
 CC systemic amyloidosis found in long-term haemodialysis patients.

XX Sequence 10 AA;

Query Match 100.0%; Score 10; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 5,1e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10

DB 1 hhqklvffaq 10

RESULT 2

AAW01414

ID AAW01414 standard; Protein; 28 AA.

AC AAW01414;

DT 20-JAN-1997 (first entry)

DE Beta/A4-amyloid peptide residues 1-28 Dutch.

XX Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;  
 KW Alzheimer's disease; stimulation; investigation; pathogenesis;  
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;  
 KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;  
 KW hemorrhage.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 22 /note= "wild type Glu subst. with Gln"

FT WO9615799-A1.

XX 30-MAY-1996.

XX

PF 22-NOV-1995; 95WO-US15007.  
 XX  
 PR 22-NOV-1994; 94US-0347144.  
 XX  
 PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

XX Anderson S;

XX WPI; 1996-268332/27.

XX Use of agents which bind beta-amyloid peptide - for diagnosis,  
 PT prevention and treatment of vascular damage caused by amyloid  
 PT deposits, partic. in haemorrhaging and Alzheimer's disease

XX Example 1; Fig 1; 52pp; English.

XX To investigate the effects of beta-amyloid peptide (BAP) on  
 CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.  
 CC One peptide contained 42 amino acids and corresp. to the full  
 CC length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained  
 CC the 28 N-terminal residues of the BAP found in Alzheimer's disease  
 CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type  
 CC (HCHWA-D), respectively. In an assay to determine the effect of  
 CC the peptides on t-PA activation, each peptide (AAR95248, 49 and 50)  
 CC gave 1st order rate constant of activation (k(app)) values of  
 CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null  
 CC and fibrinogen controls. The results demonstrate that the BAP are  
 CC able to stimulate t-PA activity in vitro, which is significant in  
 CC that it provides a means for investigating and controlling the  
 CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid  
 CC angiopathy related cerebral haemorrhage.

XX Sequence 28 AA;

Query Match 100.0%; Score 10; DB 17; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10

DB 13 hhqklvffaq 22

RESULT 3

AAB35600

ID AAB35600 standard; peptide; 28 AA.

AC AAB35600;

DT 15-FEB-2001 (first entry)

DE Human clone E22Q B(1-28) amyloid B peptide.

XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;  
 KW acute cardiovascular disease; therapy.

XX Homo sapiens.

XX US6136548-A.

XX 24-OCT-2000.

XX 02-SEP-1999; 99US-0388890.

XX 26-JUL-1996; 96US-0686959.

XX 22-NOV-1994; 94US-0347144.

XX 22-NOV-1995; 95WO-US15007.

XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

XX Anderson S;

XX

DR WPI; 2001-030939/04.  
 XX Identifying mutant tissue-type plasminogen activator (t-PA) for  
 PT improving thrombolytic therapy or treating vascular hemorrhaging, by  
 PT determining whether t-PA binds to fibrin but not to a beta amyloid  
 PT peptide  
 XX Example 3; Column 26; 23pp; English.  
 PS The present invention describes a method for identifying mutant  
 CC derivatives of tissue-type plasminogen activator, which involves  
 CC determining whether or not they bind to beta-amyloid peptides and fibrin.  
 CC Mutants will only bind to the latter. These mutants are useful in  
 CC improved thrombolytic therapies, in the treatment of Alzheimer's disease  
 CC and in the treatment of acute cardiovascular disease, which may be caused  
 CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.  
 XX  
 SQ Sequence 28 AA;

Query Match 100.0%; Score 10; DB 22; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.00012;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 Db 13 hhqklvffaq 22

RESULT 4  
 AAB91803  
 ID AAB91803 standard; Peptide; 35 AA.

AC AAB91803;  
 DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:979.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.  
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 514; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

XX Sequence 35 AA;

Query Match 100.0%; Score 10; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 Db 8 hhqklvffaq 17

RESULT 5  
 AAB91830  
 ID AAB91830 standard; Peptide; 35 AA.

AC AAB91830;

DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:1006.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.  
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 524; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 35 AA;

Query Match 100.0%; Score 10; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 0.00014;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 |||||  
 Db 8 hhqklvffaq 17

RESULT 6  
 AAW47232  
 ID AAW47232 standard; peptide; 40 AA.  
 AC AAW47232;  
 XX  
 DT 22-MAY-1998 (first entry)  
 XX  
 DE Beta-amyloid peptide fragment.  
 XX

KW Screening assay; beta-amyloid peptide; treatment;  
 KW amyloidosis disease; Alzheimer's disease.  
 XX Homo sapiens.  
 XX  
 PN US5721106-A.  
 XX  
 PD 24-FEB-1998.  
 XX  
 PF 12-SEP-1994; 94US-0304585.  
 XX  
 PR 12-SEP-1994; 94US-0304585.  
 PR 13-AUG-1991; 91US-0744767.  
 XX

PA (HARD ) HARVARD COLLEGE.  
 PA (MINU ) UNIV MINNESOTA.  
 PI Maggio JE, Mantyh PW;  
 XX WPI; 1998-168404/15.  
 XX  
 XX New in vitro screening assay for Alzheimer's disease drugs -  
 PT comprises assessing binding of labelled beta-amyloid peptide to silk  
 PT sample  
 XX  
 PS Disclosure; Columns 31-32; 36pp; English.  
 XX  
 CC The present sequence was used in the development of a novel in  
 CC vitro screening assay for agents capable of affecting the  
 CC deposition of beta-amyloid peptide (BAP) on tissue. The method  
 CC comprises contacting a silk sample with labelled BAP, optionally  
 CC in the presence of a test agent, detecting the amount of label  
 CC bound to the silk and assessing the effect of the agent on the  
 CC deposition of BAP. Agents that inhibit binding of BAP to silk are  
 CC potentially useful for treating amyloidosis diseases, especially  
 CC Alzheimer's disease.  
 XX  
 SQ Sequence 40 AA;

Query Match 100.0%; Score 10; DB 19; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HHQKLVFFAQ 10  
 |||||  
 Db 13 hhqklvffaq 22

RESULT 7  
 AAR55697  
 ID AAR55697 standard; Protein; 53 AA.  
 XX  
 AC AAR55697;  
 XX  
 DT 29-DEC-1994 (first entry)  
 XX  
 DE Sequence of unidentified protein sequence ID number 22.  
 XX  
 KW Amyloid precursor protein; APP; plaque; beta/A4; Alzheimers;  
 KW transgene; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9412627-A.  
 XX  
 PD 09-JUN-1994.  
 XX  
 PF 24-NOV-1993; 93WO-US11480.  
 XX  
 PR 25-NOV-1992; 92US-0989850.  
 PR 09-NOV-1993; 93US-0149222.  
 XX

PA (CEPH-) CEPHALON INC.  
 XX  
 PI Howland DS, Scott RW;  
 XX  
 DR WPI; 1994-200256/24.  
 XX  
 PT Transgenic animal model for Alzheimer's disease - contains  
 PT transgene encoding amyloid protein under transcriptional control  
 PT of synapsin gene promoter  
 XX  
 PS Example; Page 55; 94pp; English.  
 XX

CC There was no apparent reference to sequence ID numbers 20, 21 or 22  
 CC in the specification. The specification describes a transgenic  
 CC animal model for Alzheimer's disease. A transgenic animal  
 CC harbouring a transgene coding for an amyloid protein under the  
 CC control of a promoter is claimed. The amyloid protein can be  
 CC APP695, APP751 or APP770. The coding sequence may contain a  
 CC mutation, including the hereditary cerebral haemorrhage with  
 CC amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's  
 CC disease (FAD). Perhaps SQ IDs 20-22 corresp. to wt, HCHWA-DT  
 CC and FAD?  
 XX  
 SQ Sequence 53 AA;

Query Match 100.0%; Score 10; DB 15; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 |||||  
 Db 17 hhqklvffaq 26

RESULT 8  
 AAW26511  
 ID AAW26511 standard; Peptide; 63 AA.  
 XX  
 AC AAW26511;  
 XX  
 DT 06-JAN-1998 (first entry)



XX  
DE Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).  
XX  
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;  
KW substrate; mutin; secretase; Alzheimer's disease;  
KW hereditary cerebral haemorrhage with amyloidosis; human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 10..51  
FT /label= BAP(E22Q)  
FT /note= "beta-amyloid protein E22Q mutant"  
FT Cleavage-site 25..26  
FT /note= "secretase cleavage site"  
FT Domain 38..61  
FT /label= Transmembrane  
XX  
PN US5656477-A.  
XX  
PD 12-AUG-1997.  
XX  
PF 01-MAY-1992; 92US-0877675.  
XX  
PR 20-SEP-1993; 93US-0123659.  
PR 01-MAY-1992; 92US-0877675.  
PR 01-MAY-1992; 92US-0877675.  
XX  
PA (AMCY ) AMERICAN CYANAMID CO.  
XX  
PI Jacobsen JS, Vitek MP;  
XX WPI; 1997-414594/38.  
XX  
PT Nucleic acid encoding amyloid precursor mutin(s) - comprising  
PT reporter gene and coding sequence, for identifying compounds which  
PT modify the activity of proteolytic enzymes which cleave APP  
XX  
PS Disclosure; Fig 5A; 84pp; English.  
XX  
CC This peptide sequence shows the region of amyloid precursor protein  
CC (APP) that includes a beta-amyloid protein (BAP) carrying a point  
CC mutation (BAP E22Q) found in patients with hereditary cerebral  
CC haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an  
CC attempt to engineer an APP non-cleavable substrate for secretase,  
CC an APP-reporter (APP-REP) protein that carries the E22Q mutation  
CC has been expressed in recombinant host cells. This resulted in the  
CC secretion of an N-terminal fragment indistinguishable from that of  
CC APP-REP 751 (see AAW26391-94). Non-cleavable APP substrates can be  
CC used to detect other putative abnormal APP processing events. They  
CC can also be used to investigate cellular post-translational  
CC modifications to APP in order to determine the potential influence  
CC on normal secretase and abnormal BAP 'clipping' activities.  
XX  
SQ Sequence 63 AA;

Query Match 100.0%; Score 10; DB 18; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.00023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HHQKLVFFAQ 10  
Db 22 hhqklvffaq 31  
  
RESULT 9  
AAW26391  
ID AAW26391 standard; Peptide; 63 AA.  
XX  
AC AAW26391;  
XX  
DT 15-DEC-1997 (first entry)  
XX

DE Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).  
XX  
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;  
KW substrate; mutin; secretase; Alzheimer's disease;  
KW hereditary cerebral haemorrhage with amyloidosis; human.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 10..51  
FT /label= BAP(E22Q)  
FT /note= "beta-amyloid protein E22Q mutant"  
FT Cleavage-site 25..26  
FT /note= "secretase cleavage site"  
FT Domain 38..61  
FT /label= Transmembrane  
XX  
PN US5652092-A.  
XX  
PD 29-JUL-1997.  
XX  
PF 01-MAY-1992; 92US-0877675.  
XX  
PR 20-SEP-1993; 93US-0123659.  
PR 01-MAY-1992; 92US-0877675.  
PR 05-JUN-1995; 95US-0462859.  
XX  
PA (AMCY ) AMERICAN CYANAMID CO.  
XX  
PI Jacobsen JS, Vitek MP;  
XX WPI; 1997-392937/36.  
XX  
PT Screening for compounds which reduce beta-amyloid protein formation  
PT - using cells which express a construct encoding a marker and an  
PT amyloid precursor mutin derived from APP isoforms  
XX  
PS Disclosure; Fig 5A; 84pp; English.  
XX  
CC This peptide sequence shows the region of amyloid precursor protein  
CC (APP) that includes a beta-amyloid protein (BAP) carrying a point  
CC mutation (BAP E22Q) found in patients with hereditary cerebral  
CC haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an  
CC attempt to engineer an APP non-cleavable substrate for secretase,  
CC an APP-reporter (APP-REP) protein that carries the E22Q mutation  
CC has been expressed in recombinant host cells. This resulted in the  
CC secretion of an N-terminal fragment indistinguishable from that of  
CC APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be  
CC used to detect other putative abnormal APP processing events. They  
CC can also be used to investigate cellular post-translational  
CC modifications to APP in order to determine the potential influence  
CC on normal secretase and abnormal BAP 'clipping' activities.  
XX  
SQ Sequence 63 AA;  
  
Query Match 100.0%; Score 10; DB 18; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.00023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 HHQKLVFFAQ 10  
Db 22 hhqklvffaq 31  
  
RESULT 10  
AAW44746  
ID AAW44746 standard; Protein; 63 AA.  
XX  
AC AAW44746;  
XX  
DT 01-JUN-1998 (first entry)  
XX



PF 07-NOV-1994; 94EP-0117512.  
 XX  
 PR 12-NOV-1993; 93JP-0306026.  
 XX  
 PA (FARH ) HOECHST JAPAN LTD.  
 PA (FARH ) HOECHST JAPAN KK.  
 XX  
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;  
 XX  
 XX WPI; 1995-180492/24.  
 DR N-PSDB; AAQ88697.  
 XX  
 XX Transgenic animal model for Alzheimer's disease - contains DNA encoding  
 PT part of beta-amyloid precursor protein in a gene construct designed for  
 PT over-expression in various cell types  
 XX  
 XX Claim 2; Page 13; 32pp; English.  
 XX  
 XX The sequence represents a human brain beta-amyloid precursor protein  
 CC (APP) C-terminal peptide. The peptide is a Gln-22 mutant of  
 CC AAR74694. DNA encoding the peptide may be transferred, along  
 CC with a signal peptide (e.g. AAR74693) gene into somatic and germ  
 CC cells of a non-human mammal, and the resulting transgenic animal  
 CC may be used as a model for Alzheimer disease (AD). The animal  
 CC model exhibits symptoms similar to AD, producing large quantities  
 CC of APP C-terminal peptide, death of neuron cells in pyramidal  
 CC cells at cerebral amyloid regions, increases in glial cells and  
 CC deposition of abnormally phosphorylated tau protein. The animal  
 CC model may be used to develop new therapies for AD, including  
 CC gene therapy strategies.  
 XX  
 XX Sequence 99 AA;  
 SQ

Query Match 100.0%; Score 10; DB 16; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
 , | | | | | | | |  
 DB 13 hbgkivffaq 22

RESULT 13  
 AAB48493  
 ID AAB48493 standard; Peptide; 9 AA.  
 XX  
 AC AAB48493;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 XX Antifibrillogenic peptide #20.  
 DE  
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;  
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 9 /note= "C-terminal amide"  
 FT  
 XX WO200068263-A2.  
 XX  
 XX 16-NOV-2000.  
 PD  
 XX 04-MAY-2000; 2000WO-CA00515.  
 PF  
 XX 05-MAY-1999; 99US-0132592.  
 PR  
 XX (NEUR-) NEUROCHEM INC.  
 PA  
 XX

PI Chalifour R, Gervais F, Gupta A;  
 XX  
 DR WPI; 2001-031852/04.  
 XX  
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for  
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,  
 PT its isomer or peptidomimetic -  
 XX  
 XX Claim 7; Page 25; 46pp; English.  
 PS  
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used  
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of  
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are  
 CC therefore useful for treating amyloidosis disorders such as Alzheimer's  
 CC disease. Peptides AAB48474-B48496 were identified from the  
 CC glycosaminoglycan binding region and the prot-prot interaction region of  
 CC the human amyloid protein.  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 90.0%; Score 9; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9  
 | | | | | | | |  
 DB 1 hbgkivffa 9

RESULT 14  
 AAB46224  
 ID AAB46224 standard; peptide; 10 AA.  
 XX  
 AC AAB46224;  
 XX  
 DT 04-APR-2001 (first entry)  
 XX  
 XX Human APP derived immunogenic peptide #20.  
 DE  
 XX Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200072880-A2.  
 XX  
 XX 07-DEC-2000.  
 PD  
 XX 26-MAY-2000; 2000WO-US14810.  
 PF  
 XX 28-MAY-1999; 99US-0322289.  
 PR  
 XX (NEUR-) NEURALAB LTD.  
 XX  
 XX Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 PI  
 XX WPI; 2001-032104/04.  
 DR  
 XX Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid  
 PT specific antibody -  
 XX  
 XX Disclosure; Figure 19; 143pp; English.  
 PS  
 XX This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent







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OM protein - protein search, using sw model

Run on: July 18, 2002, 10:16:54 ; Search time 14.43 Seconds  
(without alignments)  
66.590 Million cell updates/sec

Title: US-09-724-842-27  
Perfect score: 10  
Sequence: 1 HHOKLVFFFA 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9	90.0	42	2 PN0512	beta-amyloid prote
2	9	90.0	57	2 E60045	Alzheimer's diseas
3	9	90.0	57	2 F60045	Alzheimer's diseas
4	9	90.0	57	2 G60045	Alzheimer's diseas
5	9	90.0	57	2 D60045	Alzheimer's diseas
6	9	90.0	57	2 A60045	Alzheimer's diseas
7	9	90.0	57	2 B60045	Alzheimer's diseas
8	9	90.0	82	2 PQ0438	Alzheimer's diseas
9	9	90.0	695	1 A49795	Alzheimer's diseas
10	9	90.0	747	2 JH0773	Alzheimer's diseas
11	9	90.0	770	2 QR0044	Alzheimer's diseas
12	8	80.0	33	2 Z3094	beta-amyloid prote
13	8	80.0	695	2 A27485	Alzheimer's diseas
14	8	80.0	695	2 S00550	Alzheimer's diseas
15	6	60.0	115	2 AE0523	conserved hypothet
16	6	60.0	152	2 T06645	hypothetical prote
17	6	60.0	156	2 B64735	yacc protein - Esc
18	6	60.0	156	2 F83495	hypothetical prote
19	6	60.0	156	2 F90644	hypothetical prote
20	6	60.0	231	2 H85138	hypothetical prote
21	6	60.0	352	2 T48903	wax synthase [impo
22	6	60.0	428	2 T48008	hypothetical prote
23	6	60.0	512	2 C91268	transcription acti
24	6	60.0	512	2 A41968	transcription acti
25	6	60.0	512	2 A86109	transcription acti
26	6	60.0	590	2 F95853	probable phosphol
27	6	60.0	763	2 S51300	probable membrane
28	6	60.0	1016	2 S30236	genome polyprotein
29	6	60.0	4427	2 PN0637	polyketide synthas

30	5	50.0	29	2 C47719	T-cell receptor al
31	5	50.0	32	2 S67962	valine--trna ligas
32	5	50.0	66	2 AE3608	hypothetical prote
33	5	50.0	75	2 S35774	T-cell receptor al
34	5	50.0	80	2 F96787	protein T4012.7 [1
35	5	50.0	86	2 B44530	T-cell receptor al
36	5	50.0	91	2 H82370	conserved hypothet
37	5	50.0	98	2 C71560	probable chitr t2
38	5	50.0	106	2 I40737	T2 protein - Chlam
39	5	50.0	110	2 A24092	T-cell receptor al
40	5	50.0	112	2 A69268	hypothetical prote
41	5	50.0	113	4 I39320	T cell receptor al
42	5	50.0	119	2 AC0080	probable dihydron
43	5	50.0	120	2 AE0892	dihydroneopterin a
44	5	50.0	123	1 H65093	probable dihydron
45	5	50.0	123	2 E91121	probable kinase [1

ALIGNMENTS

RESULT 1

PN0512  
beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999

C:Accession: PN0512

R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra

A:Reference number: PN0512; MUID:93290653

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SH1>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; amyloid

Query Match 90.0%; Score 9; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFFA 9

|||||

DB 13 HHOKLVFFFA 21

RESULT 2

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.002;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFFA 9

|||||

DB 18 HHOKLVFFFA 26

```

RESULT 3
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
   |||||
Db 18 HHQKLVFFA 26

RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
   |||||
Db 18 HHQKLVFFA 26

RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

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Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
   |||||
Db 18 HHQKLVFFA 26

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
   |||||
Db 18 HHQKLVFFA 26

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
   |||||
Db 18 HHQKLVFFA 26

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, I.E.
Biochem. Biophys. Res. Commun. 186, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; MUID:93075180

```



A:Accession: PQ0438  
 A:Molecule type: DNA  
 A:Residues: 1-82 <DAV>  
 C:Cross-references: GB:M83558; GB:M83657  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: C60045  
 A:Molecule type: mRNA  
 A:Residues: 12-68 <JOH>  
 A:Cross-references: EMBL:X56129  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 90.0%; Score 9; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9  
 |||||  
 Db 29 HHOKLVFFA 37

RESULT 9  
 A49795  
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C:Species: Macaca fascicularis (crab-eating macaque)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A49795  
 R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.  
 Am. J. Pathol. 138, 1423-1435, 1991  
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
 A:Reference number: A49795; MUID:91273117  
 A:Accession: A49795  
 A>Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <POD>  
 C:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing

Query Match 90.0%; Score 9; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9  
 |||||  
 Db 609 HHOKLVFFA 617

RESULT 10  
 JH0773  
 Alzheimer's disease amyloid beta protein precursor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
 C:Accession: JH0773  
 R:Okado, H.; Okamoto, H.  
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental  
 A:Reference number: JH0773; MUID:93129227  
 A:Accession: JH0773  
 A:Molecule type: mRNA  
 A:Residues: 1-747 <OKA>  
 A:Cross-references: GB:S52417; NID:q263150; PIDN:AAB24853.1; PID:g263151  
 A:Experimental source: larva  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid  
 F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 90.0%; Score 9; DB 2; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9  
 |||||  
 Db 661 HHOKLVFFA 669

RESULT 11  
 ORH044  
 Alzheimer's disease amyloid beta protein precursor [validated] - human  
 A:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIA inh  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562;  
 4668; A2858; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252;  
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;  
 Nucleic Acids Res. 17, 517-522, 1989  
 A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEM1>  
 A:Cross-references: EMBL:X13466  
 A:Note: alternative splice form APP(695)  
 R:Lemaire, H.G.  
 submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'VV', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CRAA31830.1; PID:g871360  
 A:Note: alternative splice form APP(695)  
 R:La Fauri, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAF>  
 A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AAC13654.1; PID:g516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila  
 A:Reference number: A33260; MUID:89392030  
 A:Accession: A33260  
 A:Molecule type: DNA  
 A:Residues: 656-737 <JOH>  
 A:Cross-references: GB:M29270; NID:q178863; PIDN:AAA51768.1; PID:g178865  
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid  
 A:Reference number: A35486; MUID:90321244  
 A:Accession: A35486  
 A:Molecule type: DNA  
 A:Residues: 672-710 <PRE1>  
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
 R:Yoshikawa, S.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 87, 257-263, 1990  
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
 A:Reference number: I39451; MUID:90236318  
 A:Accession: I39451  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-770 <YOS1>  
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616  
 A:Accession: I39451  
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-530, 'CWLMPVIPAFWEAKVGR' <YOS2>

A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615  
R;Toshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 102, 291-292, 1991  
A;Reference number: A59020; MUID:91340168  
A;Contents: annotation; erratum  
A;Note: revised physical map for reference I39451  
R;Levy, E.; Garman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine  
Science 248, 1124-1126, 1990  
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh  
A;Reference number: I39453; MUID:90260663  
A;Accession: I39453  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 636-737 <LEV>  
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620  
A;Note: a mutation with 693-Gln is presented  
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
Science 254, 97-99, 1991  
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer  
A;Reference number: I59562; MUID:92022553  
A;Accession: I59562  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 689-716, 'F', 718-737 <MUR>  
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721  
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijisman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,  
arakis, S.B.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,  
Am. J. Hum. Genet. 51, 998-1014, 1992  
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the  
A;Reference number: A44017; MUID:93035397  
A;Accession: A44017  
A;Molecule type: DNA  
A;Residues: 687-692, 'G', 694-718 <KAMI>  
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378  
A;Experimental source: familial Alzheimer disease family SB  
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)  
A;Accession: B44017  
A;Molecule type: DNA  
A;Residues: 687-718 <KAM2>  
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380  
A;Experimental source: familial Alzheimer disease family LIT  
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)  
A;Note: this sequence has a silent mutation  
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;  
Nature 325, 733-736, 1987  
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac  
A;Reference number: A03134; MUID:87144572  
A;Accession: A03134  
A;Molecule type: mRNA  
A;Residues: 1-288, 'V', 365-770 <KAN>  
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526  
A;Note: alternative splice form APP(695)  
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a  
A;Reference number: A29030; MUID:87231971  
A;Accession: A29030  
A;Molecule type: mRNA  
A;Residues: 284-288, 'E', 648-770 <ROB>  
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540  
A;Note: the authors translated the codon GAG for residue 647 as ASP  
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
Science 235, 877-880, 1987  
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
A;Reference number: A47584; MUID:87120328  
A;Accession: A47584  
A;Molecule type: mRNA  
A;Residues: 674-756, 'S', 758-770 <GOL>  
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707  
A;Experimental source: brain  
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
Science 235, 880-884, 1987  
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th

A;Reference number: A47585; MUID:87120329  
A;Accession: A47585  
A;Molecule type: mRNA  
A;Residues: 674-703 <TAN1>  
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958  
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue  
EMBO J. 7, 949-957, 1988  
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p  
A;Reference number: S02638; MUID:88296437  
A;Accession: S02638  
A;Molecule type: mRNA  
A;Residues: 672-678 <DVR>  
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N  
Nature 331, 528-530, 1988  
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc  
A;Reference number: S00707; MUID:88122640  
A;Accession: S00707  
A;Molecule type: mRNA  
A;Residues: 286-344, 'I', 365-366 <TAN2>  
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612  
A;Experimental source: promyelocytic leukemia cell line HL60  
A;Note: alternative splice form APP(751)  
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;  
Nature 331, 525-527, 1988  
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh  
A;Reference number: S00925; MUID:88122639  
A;Accession: S00925  
A;Molecule type: mRNA  
A;Residues: 1-344, 'I', 365-770 <PO2>  
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721  
A;Note: alternative splice form APP(751)  
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
Nature 331, 530-532, 1988  
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi  
A;Reference number: A38949; MUID:88122641  
A;Accession: A38949  
A;Molecule type: mRNA  
A;Residues: 287-367 <KIT>  
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611  
A;Experimental source: glioblastoma cell line  
A;Note: alternative splice form APP(770)  
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash  
Brain Res. Mol. Brain Res. 4, 121-131, 1988  
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three  
A;Reference number: A30320  
A;Accession: A30320  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 284-288, 'V', 365-770 <VIT1>  
A;Accession: B30320  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 122-288, 'V', 365-770 <VIT2>  
A;Accession: C30320  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 606-770 <VIT3>  
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,  
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease  
A;Reference number: A31087; MUID:88124954  
A;Accession: A31087  
A;Molecule type: mRNA  
A;Residues: 507-770 <ZAI>  
A;Cross-references: GB:M18734; NID:g187572; PIDN:AAA51726.1; PID:g187573  
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue  
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue  
A;Note: the cited Genbank accession number, J03594, is not in release 101.0  
R;Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,

Query Match 90.0%; Score 9; DB 1; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9  
|||||||  
DB 684 HHQKLVFFA 692

## RESULT 12

S23094  
beta-amyloid protein precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
C:Accession: S23094  
R:Kojima, S.; Omori, M., 1992  
FEBS Lett. 304, 57-60, 1992  
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase  
A:Reference number: S23094; MUID:92316198  
A:Accession: S23094  
A:Molecule type: protein  
A:Residues: 1-33 <KQJ>  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 80.0%; Score 8; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOKLVFFA 9  
|||||||  
DB 19 HOKLVFFA 26

## RESULT 13

A27485  
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
N:Alternate names: proteinase nexin II  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
C:Accession: A27485; S19727; I49485  
R:Yanada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor  
A:Reference number: A27485; MUID:88106489  
A:Accession: A27485  
A:Molecule type: mRNA  
A:Residues: 1-695 <YAN>  
A:CROSS-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085  
A:Experimental source: brain  
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.  
Biochim. Biophys. Acta 1129, 141-143, 1991  
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
A:Reference number: S19727; MUID:92096458  
A:Accession: S19727  
A:Molecule type: mRNA  
A:Residues: 1-210 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
A:CROSS-references: EMBL:X59379  
R:izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
Gene 112, 189-195, 1992  
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
A:Reference number: I49485; MUID:92209998  
A:Accession: I49485  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-19 <RES>  
A:CROSS-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329  
C:Genetics:  
A:Map position: 16C3  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 80.0%; Score 8; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOKLVFFA 9  
|||||||  
DB 610 HOKLVFFA 617

## RESULT 14

S00550  
Alzheimer's disease amyloid beta protein precursor - rat  
N:Alternate names: beta-A4 amyloid protein  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
C:Accession: S00550; A41245; A39820; S46251  
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
EMBO J. 7, 1365-1370, 1988  
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat  
A:Reference number: S00550; MUID:88312583  
A:Accession: S00550  
A:Molecule type: mRNA  
A:Residues: 1-695 <SHI>  
A:CROSS-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617  
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.  
Science 241, 223-226, 1988  
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co  
A:Reference number: A41245; MUID:88264430  
A:Accession: A41245  
A:Molecule type: protein  
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
A:Note: evidence for heparan sulfate attachment  
R:Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.  
FEBS Lett. 349, 109-116, 1994  
A:Title: The beta-A4 amyloid precursor protein binding to copper.  
A:Contents: annotation; copper binding sites  
A:Reference number: S46251; MUID:94320627  
A:Note: rat peptides were isolated but not sequenced  
R:Potempa, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
J. Biol. Chem. 266, 8464-8469, 1991  
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat  
A:Reference number: A39820; MUID:91217087  
A:Accession: A39820  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-32 <POT>  
A:Experimental source: brain  
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 80.0%; Score 8; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOKLVFFA 9  
|||||||  
DB 610 HOKLVFFA 617

## RESULT 15

AE0523  
conserved hypothetical protein STY0189 [Imported] - Salmonella enterica subsp. enteri  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: This species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AE0523  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
th, T.; Conerton, F.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se  
A:Reference number: AB0502; PMID:11677608

A;Accession: AE0523  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-115 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD01325.1; PID:g16501453; GSPDB:GN00176  
C;Genetics:  
A;Gene: STY0189

Query Match 60.0%; Score 6; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LVFFAQ 10  
|||||  
Db 59 LVFFAQ 64

Search completed: July 18, 2002, 10:18:56  
Job time: 122 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 18, 2002, 10:17:44 ; Search time 10.33 Seconds  
(without alignments)  
37.483 Million cell updates/sec

Title: US-09-724-842-27  
Perfect score: 10  
Sequence: 1 HHQKLVFFAQ 10

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	90.0	57	1 A4_PIG	Q29023 sus scrofa
2	9	90.0	57	1 A4_URDMA	Q29149 ursus marit
3	9	90.0	58	1 A4_CANFA	Q28280 canis famil
4	9	90.0	58	1 A4_RABIT	Q28748 cryptolagus
5	9	90.0	58	1 A4_SHEEP	Q28757 ovis aries
6	9	90.0	59	1 A4_BOVIN	Q28053 bos taurus
7	9	90.0	751	1 A4_SALISC	Q95241 salmirl sci
8	9	90.0	770	1 A4_HUMAN	P05067 homo sapien
9	8	80.0	770	1 A4_MOUSE	P12023 mus musculu
10	8	80.0	770	1 A4_RAT	P08592 rattus norv
11	6	60.0	115	1 YACC_ECOLI	P23838 escherichia
12	6	60.0	321	1 CVF_GUITH	O78494 guillardia
13	6	60.0	417	1 O65A_DROME	P82982 drosophila
14	6	60.0	512	1 CADC_ECOLI	P23890 escherichia
15	6	60.0	763	1 YN51_YEAST	P42843 saccharomyc
16	6	60.0	3080	1 POLG_ZYMVC	P18479 z genome po
17	6	60.0	3083	1 POLG_ZYMVS	Q06979 z genome po
18	6	60.0	4427	1 PKSL_BACSU	Q05470 bacillus su
19	5	50.0	80	1 APPL_ARATH	P30224 arabidopsis
20	5	50.0	112	1 Y145_ARCFU	O30092 archaeoglob
21	5	50.0	118	1 FOLB_HAEIN	P46362 haemophilus
22	5	50.0	122	1 FOLB_ECOLI	P31055 escherichia
23	5	50.0	152	1 SODC_ZANAE	O65174 zantedesch
24	5	50.0	191	1 YAPB_CAEEL	P52879 caenorhabd
25	5	50.0	201	1 AIAG_RABIT	P25227 cryptolagus
26	5	50.0	203	1 CHPE_PSEAE	O87005 pseudomonas
27	5	50.0	208	1 Y644_METJA	Q58060 methanococ
28	5	50.0	214	1 ACUB_BACSU	P39066 bacillus su
29	5	50.0	233	1 MTRP_HUMAN	Q15012 homo sapien
30	5	50.0	253	1 YTBQ_BACSU	P53560 bacillus su
31	5	50.0	258	1 MIP_CHLPN	Q927p3 chlamydia p
32	5	50.0	273	1 LACG_AGRRD	P29824 agrobacteri
33	5	50.0	284	1 LEP_PSEFL	P26844 pseudomonas

34	5	50.0	308	1 NOD1_RHIME	P03031 rhizobium m
35	5	50.0	332	1 C1B3_CAVPO	Q9qz20 cavia porce
36	5	50.0	334	1 Y293_BUCAI	P57380 buchnera ap
37	5	50.0	336	1 USG_AZOVI	P96199 azotobacter
38	5	50.0	380	1 FD3E_SOYBN	P48625 glycine max
39	5	50.0	416	1 TFXD_RHILT	P42726 rhizobium 1
40	5	50.0	425	1 RAFB_ECOLI	P16552 escherichia
41	5	50.0	444	1 CYB_RHOSH	Q02761 rhodobacter
42	5	50.0	446	1 SR54_MYCGE	P47154 mycoplasma
43	5	50.0	453	1 ST24_YEAST	P47154 mycoplasma
44	5	50.0	472	1 C901_ARATH	Q42569 arabidopsis
45	5	50.0	496	1 C7D9_SOYBN	O81971 glycine max

#### ALIGNMENTS

RESULT 1  
A4\_PIG STANDARD; PRT; 57 AA.  
AC Q29023;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
DE protein (Beta-APP) (A-beta)] (Fragment).  
GN APP.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Sulna; Suidae; Sus.  
ON NCBI\_TaxID=9823;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
-----  
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CC EMBL; X56127; CAA39592.1; -.  
CC HSSP; P05067; 1BA4.  
CC InterPro; IPR001868; A4\_APP.  
CC PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
CC PROSITE; PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
FT NON\_TER 1  
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 34 57 POTENTIAL.  
FT NON\_TER 57  
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;

Query Match 90.0%; Score 9; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.00065;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9

```
Db 18 HHQKLVFFA 26
|||||
RESULT 2
A4_URMSA STANDARD; PRT; 57 AA.
ID A4_URMSA
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC
CC EMBL: X56125; CAA39593.1; -
CC HSSP: P05067; 1AM4.
CC InterPro: IPR001868; A4_APP.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT NON_TER 1 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 34 57 POTENTIAL.
CC FT NON_TER 57 57
CC SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 90.0%; Score 9; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
|||||
Db 18 HHQKLVFFA 26
|||||
RESULT 3
A4_CANFA STANDARD; PRT; 58 AA.
ID A4_CANFA
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC
CC EMBL: X56128; CAA39593.1; -
CC HSSP: P05067; 1AML.
CC InterPro: IPR001868; A4_APP.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT NON_TER 1 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 34 57 POTENTIAL.
CC FT NON_TER 57 57
CC SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 90.0%; Score 9; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
|||||
Db 19 HHQKLVFFA 27
|||||
RESULT 4
A4_RABIT STANDARD; PRT; 58 AA.
ID A4_RABIT
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X56125; CAA39593.1; -
CC HSSP: P05067; 1BA4.
CC InterPro: IPR001868; A4_APP.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT NON_TER 1 1
CC CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
CC FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 35 58 POTENTIAL.
CC FT NON_TER 58 58
CC SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
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RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
DR EMBL; X56129; CAA39594.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 90.0%; Score 9; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 18 HHOKLVFFA 26

RESULT 5
A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RA peptide in dog, polar bear and five other mammals by cross-species
RA polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL; X56130; CAA39595.1; -.
DR HSSP; P05067; 1AML.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 90.0%; Score 9; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 18 HHOKLVFFA 26

RESULT 6
A4_BOVIN
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RA peptide in dog, polar bear and five other mammals by cross-species
RA polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL; X56124; CAA39589.1; -.
DR EMBL; X56126; CAA39591.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
```





RA Saito M., Tsukuni S., Sakaki Y.;  
RT "A novel method for making nested deletions and its application for  
RT sequencing of a 300 kb region of human APP locus.";  
RL Nucleic Acids Res. 25:1802-1808(1997).  
RN [5]  
RX SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
RP MEDLINE-88122640; PubMed-2893290;  
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
RA Gusella J.F., Neve R.L.;  
RT "Protease inhibitor domain encoded by an amyloid protein precursor  
RT mRNA associated with Alzheimer's disease.";  
RL Nature 331:528-530(1988).  
RN [6]  
RX SEQUENCE OF 287-367 FROM N.A.  
RP MEDLINE-88122641; PubMed-2893291;  
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
RT "Novel precursor of Alzheimer's disease amyloid protein shows  
RT protease inhibitory activity.";  
RL Nature 331:530-532(1988).  
RN [7]  
RX SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
RP MEDLINE-87231971; PubMed-3035574;  
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
RT "Molecular cloning and characterization of a cDNA encoding the  
RT cerebrovascular and the neuritic plaque amyloid peptides.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
RN [8]  
RX SEQUENCE OF 507-770 FROM N.A.  
RP MEDLINE-88124954; PubMed-2893379;  
RA Zein S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
RA Marotta C.A.;  
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
RT disease brain: coding and noncoding regions of the fetal precursor  
RT mRNA are expressed in the cortex.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
RN [9]  
RX SEQUENCE OF 672-681.  
RP MEDLINE-88035004; PubMed-3312495;  
RA Farbridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
RA Tourtellotte W.W., Huebner V., Shively J.E.;  
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
RT microvessels.";  
RL J. Neurochem. 49:1394-1401(1987).  
RN [10]  
RX SEQUENCE OF 739-770 FROM N.A.  
RP MEDLINE-90236318; PubMed-2110105;  
RA Yoshikai S.-I., Sakaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
RT "Genomic organization of the human amyloid beta-protein precursor  
RT gene.";  
RL Gene 87:257-263(1990).  
RN [11]  
RX SEQUENCE OF 1-10 FROM N.A.  
RP TISSUE=Liver;  
RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
RT encodes a 95-kDa polypeptide.";  
RL Nucleic Acids Res. 16:9351-9351(1988).  
RN [12]  
RX SEQUENCE OF 18-50.  
RP MEDLINE-87350462; PubMed-3597385;  
RA van Nostrand W.E., Cunningham D.D.;  
RT "Purification of protease nexin II from human fibroblasts.";  
RL J. Biol. Chem. 262:8508-8514(1987).  
RN [13]  
RX IDENTITY OF APP WITH NEXIN-II.  
RA MEDLINE-89384866; PubMed-2506449;  
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
RA Sinha S.;  
RT "The secreted form of the Alzheimer's amyloid precursor protein with  
RT the Kunitz domain is protease nexin-II.";

RL Nature 341:144-147(1989).  
RN [14]  
RX PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
RP MEDLINE-90211252; PubMed-1969731;  
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
RT disease amyloid protein precursor.";  
RL Biochem. Biophys. Res. Commun. 167:716-721(1990).  
RN [15]  
RX COMPLEX WITH G(O).  
RP MEDLINE-93188965; PubMed-8446172;  
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,  
RA Murayama Y., Ogata E.;  
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
RT protein G(O).";  
RL Nature 362:75-79(1993).  
RN [16]  
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
RP MEDLINE-99215582; PubMed-10201399;  
RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,  
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
RA Parker M.W.;  
RT "Crystal structure of the N-terminal, growth factor-like domain of  
RT Alzheimer amyloid precursor protein.";  
RL Nat. Struct. Biol. 6:327-331(1999).  
RN [17]  
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
RP MEDLINE-91104913; PubMed-2125487;  
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;  
RT "X-ray crystal structure of the protease inhibitor domain of  
RT Alzheimer's amyloid beta-protein precursor.";  
RL Biochemistry 29:10018-10022(1990).  
RN [18]  
RX STRUCTURE BY NMR OF 289-344.  
RP MEDLINE-92031488; PubMed-1718421;  
RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,  
RA Kmarack M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
RA Tamburini P.P.;  
RT "Sequential NMR resonance assignment and structure determination of  
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
RT precursor protein.";  
RL Biochemistry 30:10467-10478(1991).  
RN [19]  
RX STRUCTURE BY NMR OF 672-699.  
RP MEDLINE-94281210; PubMed-7516706;  
RA Talafofus J., Marcinkowski K.J., Klopman G., Zagorski M.G.;  
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";  
RL Biochemistry 33:7788-7796(1994).  
RN [20]  
RX STRUCTURE BY NMR OF 696-706.  
RP MEDLINE-97128622; PubMed-8973180;  
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
RT membrane-mimicking environment";  
RL Biochemistry 33:16094-16104(1996).  
RN [21]  
RX STRUCTURE BY NMR OF 672-711.  
RP MEDLINE-98359733; PubMed-96933002;  
RA Coles M., Bicknell W., Watson A.A., Craik D.J.;  
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle  
RT environment. Is the membrane-spanning domain where we think it is?";  
RL Biochemistry 37:11064-11077(1998).  
RN [22]  
RX STRUCTURE BY NMR OF 672-699.  
RP MEDLINE-20400056; PubMed-10940222;  
RA Poulsen S.A., Watson A.A., Craik D.J.;  
RT "Solution structures in aqueous SDS micelles of two amyloid beta  
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
RT site.";  
RL J. Struct. Biol. 130:142-152(2000).  
RN [23]  
RX STRUCTURE BY NMR OF 681-706.  
RP MEDLINE-20400055; PubMed-10940221;

RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,  
RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;  
RA "The Alzheimer's peptide a beta adopts a collapsed coil structure in  
RT water.";  
RL J. Struct. Biol. 130:130-141(2000).  
RN [24]  
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.  
RX MEDLINE=88296437; PubMed=2900137;  
RA Dyke T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,  
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;  
RT "Identification, transmembrane orientation and biogenesis of the  
RT amyloid A4 precursor of Alzheimer's disease.";  
Query Match 90.0%; Score 9; DB 1; Length 770;  
Best Local Similarity 100.0%; Pred. No. 0.0054;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HHQKLVFFA 9  
Db 684 HHQKLVFFA 692  
RESULT 9  
A4\_MOUSE  
ID A4\_MOUSE STANDARD; PRT; 770 AA.  
AC P12023;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog precursor  
DE (Amyloidogenic glycoprotein) (AG).  
GN APP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OM Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
RC STRAIN-BALB/C; TISSUE-Brain;  
RX MEDLINE=92096458; PubMed=1756177;  
RA de Strooper B., van Leuven F., van den Bergh H.;  
RT "The amyloid beta protein precursor or proteinase nexin II from mouse  
RL is closer related to its human homolog than previously reported.";  
RL Biochim. Biophys. Acta 1129:141-143(1991).  
RN [2]  
RN SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
RC TISSUE-Brain;  
RX MEDLINE=88106489; PubMed=3322280;  
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;  
RT "Complementary DNA for the mouse homolog of the human amyloid beta  
RL protein precursor.";  
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
RN [3]  
RN REVISIONS.  
RA Yamada T.;  
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN SEQUENCE OF 289-364 FROM N.A.  
RC STRAIN-CD-1; TISSUE-Placenta;  
RX MEDLINE=89345111; PubMed=2569710;  
RA Fukuchi K., Martin G.M., Deeb S.S.;  
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
RT precursor of Mus domesticus.";  
RL Nucleic Acids Res. 17:5396-5396(1989).  
RN [5]  
RN SEQUENCE OF 1-19 FROM N.A.  
RX MEDLINE=9220998; PubMed=1555768;  
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
RA Sakai Y.;  
RT "Positive and negative regulatory elements for the expression of the  
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
RL Gene 112:189-195(1992).  
RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
RX TISSUE=Brain, and Kidney;  
RX MEDLINE=89149813; PubMed=2493250;  
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;  
RT "Structure and expression of the alternatively-spliced forms of mRNA  
RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
RT precursor.";  
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),  
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS  
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND  
CC LIVER.  
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
CC PHOSPHORYLATION (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
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CC -----  
CC EMBL; X59379; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; M18373; AAA37139.1; -;  
DR EMBL; X15210; CAA33280.1; -;  
DR EMBL; D10603; BAA01456.1; -;  
DR EMBL; M24397; AAA39929.1; -;  
DR PIR; A27485; A27485.  
DR PIR; S04855; S04855.  
DR PIR; S19727; S19727.  
DR HSP; P05067; IQCM.  
DR MGD; MGI:88059; App.  
DR InterPro; IPR001868; A4\_APP.  
DR InterPro; IPR002223; Kunitz\_BPTI.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00014; Kunitz\_BPTI; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00759; BASICPTASE.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR SMART; SM00131; KU; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PS02079; BPTI\_KUNITZ\_2; 1.  
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
KW Alternative splicing; Serine protease inhibitor.  
FT SIGNAL 1 17  
FT CHAIN 18 770  
FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN  
FT HOMOLOG.  
FT DOMAIN 18 699  
FT EXTRACELLULAR (POTENTIAL).  
FT POTENTIAL.  
FT TRANSMEM 700 723  
FT CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 724 770  
FT EQUIVALENT OF BETA-AMYLOID PROTEIN.  
FT DOMAIN 673 715  
FT BPTI/KUNITZ INHIBITOR.  
FT DOMAIN 287 345  
FT SITE 759 762  
FT CLATHRIN-BINDING (BY SIMILARITY).  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT E -> V (IN ISOFORM APP(695)).  
FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN  
FT MISSING (IN ISOFORM APP(695)).  
FT VARSPLIC 290 364  
FT VARSPLIC 346 380  
FT MISSING (IN ISOFORM APP(751)).  
FT VARSPLIC 396 770  
FT AA; 86752 MW; 26C50DE0890CAFA7A CRC64;  
SQ SEQUENCE

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Query Match      80.0%; Score 8; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQKLVFFA 9
DB 685 HQKLVFFA 692

RESULT 10
A4_RAT STANDARD; PRT; 770 AA.
ID A4_RAT
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07648; CAA30488.1; -
DR EMBL; X14066; CAA32229.1; -
DR PIR; S00550; S00550.
DR PIR; S03607; S03607.
DR HSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT HOMOLOG.
FT DOMAIN 18 699
FT TRANSMEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 759 762
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT VARSPLIC 289 289
FT VARSPLIC 290 364
SQ SEQUENCE 770 AA; 86704 MW; C26C9D68B2D929A7 CRC64;

Query Match      80.0%; Score 8; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQKLVFFA 9
DB 685 HQKLVFFA 592

RESULT 11
YACC_ECOLI STANDARD; PRT; 115 AA.
ID YACC_ECOLI
AC P23838; P75654;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yacc precursor.
GN YACC OR B0122.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89327155; PubMed=2666401;
RA Xie Q.W., Tabor C.W., Tabor H.;
RT "Spermidine biosynthesis in Escherichia coli: promoter and
RT termination regions of the speed operon.";
RL J. Bacteriol. 171:4457-4465(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / W3110;
RX MEDLINE=94261430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishihama A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
RT the 2.4-4.1 min (110,917-193,643 bp) region.";
RL Nucleic Acids Res. 22:1637-1639(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1233-1244(1997).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J02804; AAA24642.1; -
CC EMBL: D26562; CAB20296.1; -
CC EMBL: AE000121; AAC73233.1; ALT_INIT.
CC PIR: A33863; A33863.
CC PIR: S45199; S45199.
CC EcoGene: EGI1089; Yacc.
CC Hypothetical protein: Signal; Complete proteome.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 115 HYPOTHETICAL PROTEIN YACC.
CC SEQUENCE 115 AA; 12854 MW; C078DD2653221EC9 CRC64;
CC -----
CC Query Match 60.0%; Score 6; DB 1; Length 115;
CC Best Local Similarity 100.0%; Pred. No. 2.3;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 5 LVFFAQ 10
CC DB 59 LVFFAQ 64
CC -----
CC RESULT 12
CC CYF_GUITH STANDARD; PRT; 321 AA.
CC AC 078494:
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Apocytochrome F precursor.
CC GN PETA.
CC OS Guillardia theta (Cryptomonas phi).
CC OG Chloroplast.
CC OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
CC OX NCBI_TaxID=55529;
CC [1]
CC SEQUENCE FROM N.A.
CC RA Douglas S.E., Penny S.L.;
CC RA "The plastid genome of the cryptophyte alga, Guillardia theta:
CC complete sequence and conserved synteny groups confirm its common
CC ancestry with red algae.";
CC RL J. Mol. Evol. 48:236-244(1999).
CC CC -1- FUNCTION: TRANSLOCATES PROTONS ACROSS THE THYLAKOID MEMBRANE AND
CC TRANSFERS ELECTRONS FROM PHOTOSYSTEM II TO PHOTOSYSTEM I. IT
CC RECEIVES ELECTRONS FROM THE RIESKE IRON-SULFUR PROTEIN AND PASSES
CC THEM TO PLASTOCYANIN; THIS FUNCTION IS VERY SIMILAR TO THAT OF
CC MITOCHONDRIAL CYTOCHROME C1.
CC CC -1- SUBUNIT: MEMBER OF THE CYTOCHROME B6/F COMPLEX INCLUDING
CC CYTOCHROME B6, CYTOCHROME F AND PROBABLY AN IRON SULFUR PROTEIN.
CC CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane (Probable).
CC CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C FAMILY.
CC -----
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CC -----
CC EMBL: AF041468; AAC35685.1; -
CC HSSP: P36438; 1HCZ.
CC DR InterPro; IPR002325; Apocyt.F.
CC DR InterPro; IPR000345; CytC_heme_bind.

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DR Pfam; PF01333; Apocytochrome_F; 1.
DR PRINTS; PR00610; CYTOCHROME_F.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR KW Electron transport; Heme; Chloroplast; Thylakoid;
KW Photosynthesis; Photosystem I; Photosystem II; Transist peptide;
KW Transmembrane.
FT TRANSIT 1 38 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 39 321 APOCYTOCHROME F.
FT BINDING 59 59 HEME (COVALENT) (PROBABLE).
FT BINDING 62 62 HEME (COVALENT) (PROBABLE).
FT METAL 63 63 IRON (HEME AXIAL LIGAND) (PROBABLE).
FT TRANSMEM 287 307 POTENTIAL.
FT SEQUENCE 321 AA; 35173 MW; 42A1FF89FB05AE3D CRC64;
CC -----
CC Query Match 60.0%; Score 6; DB 1; Length 321;
CC Best Local Similarity 100.0%; Pred. No. 5.4;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 2 HOKLVF 7
CC DB 161 HOKLVF 166
CC -----
CC RESULT 13
CC O65A_DROME STANDARD; PRT; 417 AA.
CC ID O65A_DROME
CC AC P82982;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Putative odorant receptor 65a.
CC GN OR65A.
CC OS Drosophila melanogaster (Fruit fly).
CC OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_TaxID=7227;
CC [1]
CC SEQUENCE FROM N.A.
CC RP STRAIN=BERKELEY.
CC RX MEDLINE=20196006; PubMed=10731132;
CC RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
CC Ananthanides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallie R.F.,
CC George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
CC Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
CC Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
CC Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
CC Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
CC Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
CC Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
CC Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
CC Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
CC Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
CC de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
CC Dodson K., Dou L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
CC Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
CC Folsler K.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
CC Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
CC Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
CC Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
CC Jalali M., Kalush F., Karpen C.H., Ke Z., Kennison J.A., Ketchum K.A.,
CC Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
CC Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
CC Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
CC Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
CC Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
CC Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paciej J.M.,
CC Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,
CC Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
CC Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
CC Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
CC Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhao G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
"The genome sequence of *Drosophila melanogaster*."  
Science 287:2185-2195(2000).  
[2]  
RN CONCEPTUAL TRANSLATION.  
RP Robertsson H.M.:  
RL Unpublished observations (MAY-2001).  
CC -|- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT RECEPTOR.  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -|- SIMILARITY: BELONGS TO DROSOPHILA ODORANT RECEPTOR FAMILY OF G-PROTEIN COUPLED RECEPTORS.  
CC -|- CAUTION: REF.1 SEQUENCE DIFFERS AT SEVERAL POSITIONS FROM THAT SHOWN DUE TO DIFFERENCES IN THE PREDICTION OF SPLICE SITES.  
-----  
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-----  
DR EMBL; AE003563; -; NOT\_ANNOTATED\_CDS.  
DR FlyBase; FBgn041625; O-65a.  
KW Hypothetical protein; Transmembrane; G-protein coupled receptor;  
KW Olfaction; Multigene family.  
FT DOMAIN 1 62 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 63 83 1 (POTENTIAL).  
FT DOMAIN 84 98 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 99 119 2 (POTENTIAL).  
FT DOMAIN 120 152 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 153 173 3 (POTENTIAL).  
FT DOMAIN 174 206 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 207 227 4 (POTENTIAL).  
FT DOMAIN 228 290 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 291 311 5 (POTENTIAL).  
FT DOMAIN 312 316 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 317 337 6 (POTENTIAL).  
FT DOMAIN 338 393 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 394 414 7 (POTENTIAL).  
FT DOMAIN 415 417 CYTOPLASMIC (POTENTIAL).  
SQ SEQUENCE 417 AA; 48730 MW; 2112BE9E1E356059 CRC64;  
  
Query Match 60.0%; Score 6; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 LVFFAQ 10  
Db 112 LVFFAQ 117  
  
RESULT 14  
CAD\_CAD\_ECOLI STANDARD; PRT; 512 AA.  
AC P23890;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Transcriptional activator cadC.  
GN CAD\_C OR B4133.  
OS *Escherichia coli*.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC *Escherichia*.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.

MEDLINE=92105022; PubMed=1370290;  
Watson N., Dnyak D.S., Rosey E.L., Slonczewski J.L., Olson E.R.;  
"Identification of elements involved in transcriptional regulation of the *Escherichia coli* cad operon by external pH."  
J. Bacteriol. 174:530-540(1992).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=K12 / MG1655;  
RX MEDLINE=95334362; PubMed=7610040;  
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L., Blattner F.R.:  
"Analysis of the *Escherichia coli* genome VI: DNA sequence of the region from 92.8 through 100 minutes."  
Nucleic Acids Res. 23:2105-2119(1995).  
RL NUCLEIC ACIDS RES. 23:2105-2119(1995).  
CC -|- FUNCTION: REQUIRED FOR PCAD INDUCTION, A PROMOTER UPSTREAM OF CADB THAT IS RESPONSIBLE FOR THE PH-REGULATED EXPRESSION OF CADB.  
CC -|- SIMILARITY: TO V.CHOLERAE TOXR, AND TO THE C-TERMINI OF A GROUP OF TRANSCRIPTIONAL ACTIVATORS (OMPR-LIKE PROTEINS).  
-----  
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-----  
DR EMBL; M67452; AAA23531.1; -;  
DR EMBL; U14003; AAA97033.1; -;  
DR EMBL; AF000486; AAC77094.1; -;  
DR PIR; C41968; G41968.  
DR Ecogene; EGI0133; cadC.  
DR InterPro; IPR001440; TPR.  
DR InterPro; IPR001867; Trans\_reg\_C.  
DR Pfam; PF00486; Trans\_reg\_C; 1.  
KW Transcription regulation; DNA-binding; Activator; Transmembrane;  
KW Trans-acting factor; Complete proteome.  
FT TRANSMEM 155 180 POTENTIAL.  
SQ SEQUENCE 512 AA; 57813 MW; AA19F5E1D293ACCF CRC64;  
  
Query Match 60.0%; Score 6; DB 1; Length 512;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 LVFFAQ 10  
Db 37 LVFFAQ 42  
  
RESULT 15  
YNS1\_YEAST STANDARD; PRT; 763 AA.  
AC P42843;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 83.9 kDa protein in RPA2-STB1 intergenic region.  
GN YNL311C OR N0376.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=S288C / FY1676;  
RX MEDLINE=96076632; PubMed=7502583;  
RA Maftahi M., Nicaud J.-M., Levesque H., Gaillardin C.;  
"Sequencing analysis of a 24.7 kb fragment of yeast chromosome XIV identifies six known genes, a new member of the hexose transporter family and ten new open reading frames."  
Yeast 11:1077-1085(1995).  
[2]  
RN

```

RP SEQUENCE OF 149-763 FROM N.A.
RA Maurer C.T.C., Urbanus J.H.M., Planta R.J.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z46259; CAA86384.1; -.
CC EMBL; Z71587; CAA96240.1; -.
CC SGD; S0005255; YNL311C.
CC InterPro: IPR001810; F-box.
CC Pfam: PF00646; F-box; 1.
CC SMART; SM00256; FBOX; 1.
CC PROSITE; PS50181; FBOX; 1.
CC KW Hypothetical protein.
CC FT DOMAIN 54 100 F-BOX.
CC FT DOMAIN 22 28 POLY-GLU.
CC SQ SEQUENCE 763 AA; 88941 MW; 81102168449051BC CRC64;

Query Match 60.0%; Score 6; DB 1; Length 763;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLV 6
Db 323 HHQKLV 328

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Search completed: July 18, 2002, 10:19:45  
Job time: 121 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 18, 2002, 10:17:24 ; Search time 25.04 Seconds  
(without alignments)  
69.087 Million cell updates/sec

Title: US-09-724-842-27

Perfect score: 10

Sequence: 1 HHQKLVFFAQ 10

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_19.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	9	90.0	28	4	Q9UCD1	Q9ucd1 homo sapien
2	9	90.0	30	4	Q9UCA9	Q9uca9 homo sapien
3	9	90.0	33	4	Q9UC33	Q9uc33 homo sapien
4	9	90.0	82	4	P78438	P78438 homo sapien
5	9	90.0	82	4	Q16014	Q16014 homo sapien
6	9	90.0	82	4	Q16019	Q16019 homo sapien
7	9	90.0	82	4	Q16020	Q16020 homo sapien
8	9	90.0	97	4	Q13778	Q13778 homo sapien
9	9	90.0	534	13	O93296	O93296 gallus gall
10	9	90.0	569	13	Q9PVL1	Q9pvl1 gallus gall
11	9	90.0	693	13	Q98SG0	Q98sg0 xenopus lae
12	9	90.0	695	6	Q95KN7	Q95kn7 macaca fasc
13	9	90.0	695	11	O60496	O60496 cavia sp. p
14	9	90.0	695	13	Q9DGJ8	Q9dgj8 gallus gall
15	9	90.0	695	13	Q98SF9	Q98sf9 xenopus lae
16	9	90.0	747	13	Q91963	Q91963 xenopus. ap

17	9	90.0	751	13	Q9DGJ7	Q9dgj7 gallus gall
18	9	90.0	770	6	Q9TU10	Q9tu10 sus scrofa
19	9	90.0	780	13	O73683	O73683 tetraodon f
20	8	80.0	79	11	O35463	O35463 cricetus
21	8	80.0	607	11	O99K32	O99k32 mus musculus
22	8	80.0	612	13	Q919E7	Q919e7 brachydanio
23	8	80.0	695	11	P97487	P97487 mus musculus
24	8	80.0	699	13	O57394	O57394 narke japon
25	8	80.0	737	13	O93279	O93279 fugu rubrip
26	8	80.0	738	13	Q90W28	Q90w28 brachydanio
27	7	70.0	19	4	Q9UCC8	Q9ucc8 homo sapien
28	6	60.0	152	10	Q9ST29	Q9st29 arabidopsis
29	6	60.0	231	10	Q8SV79	Q8sv79 arabidopsis
30	6	60.0	352	10	Q9XGY6	Q9xgy6 simmondsia
31	6	60.0	428	10	Q9M1Q8	Q9m1q8 arabidopsis
32	6	60.0	461	12	O89329	O89329 zucchini ye
33	6	60.0	574	17	Q9HJC7	Q9hjc7 thermoplasma
34	6	60.0	590	16	Q92X68	Q92x68 rhizobium m
35	6	60.0	623	5	Q9VBV8	Q9vbv8 drosophila
36	6	60.0	1016	12	Q05912	Q05912 zucchini ye
37	5	50.0	14	4	Q9UH91	Q9uh91 homo sapien
38	5	50.0	15	5	Q9TW5	Q9tw5 artemia (br
39	5	50.0	34	2	O9ZG38	O9zg38 chlamydia t
40	5	50.0	34	8	Q9XQR5	Q9xqr5 pisum sativ
41	5	50.0	55	5	Q9NMJ6	Q9nmj6 leishmania
42	5	50.0	91	16	Q9KVT2	Q9kvt2 vibrio chol
43	5	50.0	94	16	Q9AOW1	Q9aow1 streptococc
44	5	50.0	98	16	O84083	O84083 chlamydia t
45	5	50.0	100	8	O99895	O99895 microarthri

#### ALIGNMENTS

RESULT 1  
Q9UCD1 ID Q9UCD1 PRELIMINARY; PRT; 28 AA.  
AC Q9UCD1;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE BETA-AMYLOID PEPTIDE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94045685; PubMed=82290004;  
RA Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;  
RT "Characterization of beta-amyloid peptide from human cerebrospinal fluid.";  
RL J. Neurochem. 61:1965-1968(1993).  
DR HSSP; P05067; LAMB. 3244 MW; DE7BD081160AFC81 CRC64;  
SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;

Query Match	90.0%;	Score 9;	DB 4;	Length 28;
Best Local Similarity	100.0%;	Pred. No. 0.0012;		
Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;	Caps 0;
QY 1 HHQKLVFFA 9				
Db 13 HHQKLVFFA 21				
RESULT 2				
Q9UCA9 ID Q9UCA9 PRELIMINARY; PRT; 30 AA.				
AC Q9UCA9;				
DT 01-MAY-2000 (Tremblrel. 13, Created)				
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)				
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)				

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DE BETA-AMYLOID PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94153015; PubMed=8109908;
RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT "The amino acid sequence of neuritic plaque amyloid from a familial
RT Alzheimer's disease patient.";
RL Ann. Neurol. 35:245-246(1994).
DR HSP; P05067; IBA4.
SQ SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;

Query Match          90.0%; Score 9; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 13 HHOKLVFFA 21

RESULT 3
Q9UC33          PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RL Nature 359:325-327(1992).
DR HSP; P05067; IBA4.
SQ SEQUENCE 33 AA; 3674 MW; B1DFE2F4167ABD0 CRC64;

Query Match          90.0%; Score 9; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 13 HHOKLVFFA 21

RESULT 4
P78438          PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -.
DR EMBL; M29269; AAA51768.1; JOINED.
DR EMBL; M15532; AAA51564.1; -.
DR EMBL; S45136; AAB23646.1; -.
DR HSP; P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match          90.0%; Score 9; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 29 HHOKLVFFA 37

RESULT 5
Q16014          PRELIMINARY; PRT; 82 AA.
ID Q16014;
AC Q16014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match          90.0%; Score 9; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 30 HHOKLVFFA 38
```

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RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -.
DR EMBL; M29269; AAA51768.1; JOINED.
DR EMBL; M15532; AAA51564.1; -.
DR EMBL; S45136; AAB23646.1; -.
DR HSP; P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match          90.0%; Score 9; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 29 HHOKLVFFA 37

RESULT 5
Q16014          PRELIMINARY; PRT; 82 AA.
ID Q16014;
AC Q16014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match          90.0%; Score 9; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 30 HHOKLVFFA 38
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RESULT 6
Q16019 ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Derman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -.
DR HSSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

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Query Match 90.0%; Score 9; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
   | | | | | | | |
DB 30 HHQKLVFFA 38

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RESULT 7
Q16020 ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Derman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -.
DR HSSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

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Query Match 90.0%; Score 9; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
   | | | | | | | |
DB 30 HHQKLVFFA 38

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RESULT 8
Q13778 ID Q13778 PRELIMINARY; PRT; 97 AA.
AC Q13778;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RL brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
FT NON_TER 1
FT NON_TER 97
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

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Query Match 90.0%; Score 9; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
   | | | | | | | |
DB 11 HHQKLVFFA 19

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RESULT 9
O93296 ID O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
FT NON_TER 534
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

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Query Match 90.0%; Score 9; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9

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Db 448 HHQKLVFFA 456
|||||
KW Signal. 1 18 POTENTIAL.
FT SIGNAL 693 AA; 78568 MW; CAFIDF655C1AB653 CRC64;
SQ SEQUENCE 693 AA; 78568 MW; CAFIDF655C1AB653 CRC64;

Query Match 90.0%; Score 9; DB 13; Length 693;
Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 HHQKLVFFA 9
|||||
Db 607 HHQKLVFFA 615

RESULT 12
Q95KN7 PRELIMINARY; PRT; 695 AA.
ID Q95KN7
AC Q95KN7
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlinsky M.B., Tolan D.R., Seikoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M59727; AAA36829.1; -. POTENTIAL.
FT SIGNAL 1 17
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 90.0%; Score 9; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 HHQKLVFFA 9
|||||
Db 609 HHQKLVFFA 617

RESULT 13
Q60496 PRELIMINARY; PRT; 695 AA.
ID Q60496
AC Q60496
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; IBA4.
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```
Db 448 HHQKLVFFA 456
|||||
KW Signal. 1 18 POTENTIAL.
FT SIGNAL 693 AA; 78568 MW; CAFIDF655C1AB653 CRC64;
SQ SEQUENCE 693 AA; 78568 MW; CAFIDF655C1AB653 CRC64;

Query Match 90.0%; Score 9; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
|||||
Db 484 HHQKLVFFA 492

RESULT 11
Q98SG0 PRELIMINARY; PRT; 693 AA.
ID Q98SG0
AC Q98SG0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -.
DR HSSP; P05067; 1HZ3.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
FT SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 90.0%; Score 9; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
|||||
Db 484 HHQKLVFFA 492

RESULT 11
Q98SG0 PRELIMINARY; PRT; 693 AA.
ID Q98SG0
AC Q98SG0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -.
DR HSSP; P05067; 1HZ3.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
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DR InterPro: IPR001868; A4\_APP.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRA; 1.  
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 90.0%; Score 9; DB 11; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9  
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Db 609 HHOKLVFFA 617

## RESULT 14

Q9DQJ8 PRELIMINARY; PRT; 695 AA.  
AC Q9DQJ8;  
DT 01-MAR-2001 (TREMELrel. 16, Created)  
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sarasa M., Rodoloso A., Sorribas V.;  
RT "Cloning of full-length chicken beta-amyloid precursor protein isoforms".  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF289218; ANG00593.1; -.  
DR HSSP: P05067; IBA4.  
DR InterPro: IPR001868; A4\_APP.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 90.0%; Score 9; DB 13; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9  
|||||

Db 609 HHOKLVFFA 617

## RESULT 15

Q98SF9 PRELIMINARY; PRT; 695 AA.  
AC Q98SF9;  
DT 01-JUN-2001 (TREMELrel. 17, Created)  
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
DE BETA-AMYLOID PRECURSOR PROTEIN B.  
GN APP.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Van den Hurk W.H.;

RL Thesis (2001), Department of Biological Sciences,  
RL University of Nijmegen, Nijmegen, Netherlands.

DR EMBL: AJ298151; CAC37194.1; -.  
DR HSSP: P05067; 1H23.  
DR InterPro: IPR001868; A4\_APP.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRA; 1.  
KW SIGNAL.  
FT SIGNAL. 1 18 POTENTIAL.  
SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;

Query Match 90.0%; Score 9; DB 13; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.015;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9  
|||||

Db 609 HHOKLVFFA 617

Search completed: July 18, 2002, 10:19:28  
Job time: 124 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:16:49 ; Search time 12.97 Seconds  
(without alignments)  
18.832 Million cell updates/sec

Title: US-09-724-842-27  
Perfect score: 10  
Sequence: 1 HHOKLVFFAQ 10

Scoring table:  
OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	28	4	US-09-388-890-12
2	10	100.0	40	1	US-08-304-585-8
3	10	100.0	63	1	US-08-462-859A-3
4	10	100.0	63	1	US-08-123-659A-3
5	10	100.0	63	1	US-08-464-247A-3
6	10	100.0	63	1	US-08-464-248A-3
7	10	100.0	99	3	US-08-339-708A-6
8	9	90.0	15	2	US-08-612-785B-37
9	9	90.0	17	4	US-08-264-709A-2
10	9	90.0	26	1	US-08-304-585-7
11	9	90.0	28	1	US-08-346-849-4
12	9	90.0	28	1	US-08-302-808-7
13	9	90.0	28	2	US-08-609-090-2
14	9	90.0	28	2	US-08-986-948-7
15	9	90.0	28	2	US-08-293-284A-4
16	9	90.0	28	2	US-08-461-216-2
17	9	90.0	28	4	US-09-388-890-2
18	9	90.0	28	4	US-09-388-890-3
19	9	90.0	28	4	US-09-388-890-4
20	9	90.0	28	4	US-09-388-890-5
21	9	90.0	28	4	US-09-388-890-6
22	9	90.0	28	4	US-09-388-890-7
23	9	90.0	28	4	US-09-388-890-8
24	9	90.0	28	4	US-09-388-890-13
25	9	90.0	28	4	US-09-388-890-14
26	9	90.0	28	4	US-09-264-709A-1
27	9	90.0	28	4	US-08-723-661B-2

28	9	90.0	30	2	US-08-609-090-3	Sequence 3, Appl1
29	9	90.0	33	2	US-08-609-090-4	Sequence 4, Appl1
30	9	90.0	35	1	US-08-304-585-6	Sequence 6, Appl1
31	9	90.0	35	2	US-08-612-785B-36	Sequence 36, Appl1
32	9	90.0	35	2	US-08-612-785B-38	Sequence 38, Appl1
33	9	90.0	35	2	US-08-612-785B-40	Sequence 40, Appl1
34	9	90.0	36	2	US-08-609-090-6	Sequence 6, Appl1
35	9	90.0	38	1	US-08-302-808-1	Sequence 1, Appl1
36	9	90.0	38	2	US-07-737-371E-68	Sequence 68, Appl1
37	9	90.0	39	1	US-08-986-948-1	Sequence 1, Appl1
38	9	90.0	39	1	US-08-304-585-5	Sequence 5, Appl1
39	9	90.0	39	1	US-08-302-808-2	Sequence 2, Appl1
40	9	90.0	39	2	US-08-609-090-7	Sequence 7, Appl1
41	9	90.0	39	2	US-08-682-245A-1	Sequence 1, Appl1
42	9	90.0	39	2	US-08-986-948-2	Sequence 2, Appl1
43	9	90.0	40	1	US-07-744-767A-1	Sequence 1, Appl1
44	9	90.0	40	1	US-08-235-400-2	Sequence 2, Appl1
45	9	90.0	40	1	US-08-476-464A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1  
US-09-388-890-12  
; Sequence 12, Application US/09388890  
; Patent No. 6136548  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, STEPHEN  
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT  
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: HOWREY & SIMON  
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: US  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/388,890  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/686,959  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: AUERBACH, JEFFREY I.  
; REGISTRATION NUMBER: 32,680  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 383-7451  
; TELEFAX: (202) 383-6610  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: YES  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: HOMO SAPIENS  
; IMMEDIATE SOURCE:  
; CLONE: E22Q B(1-28) peptide of amyloid B protein  
US-09-388-890-12

Query Match 100.0%; Score 10; DB 4; Length 28;

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Best Local Similarity 100.0%; Pred. No. 3e-05; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 HHOKLVFFAQ 10
Db 13 HHOKLVFFAQ 22

RESULT 2
US-08-304-585-8
; Sequence 8, Application US/08304585
; Patent No. 5721106
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-304-585-8

Query Match 100.0%; Score 10; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10
Db 13 HHOKLVFFAQ 22

RESULT 3
US-08-462-859A-3
; Sequence 3, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company

```

```

; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-859A-3

Query Match 100.0%; Score 10; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10
Db 22 HHOKLVFFAQ 31

RESULT 4
US-08-123-659A-3
; Sequence 3, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611

```

TELEFAX: (518)475-0619  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-123-659A-3

Query Match 100.0%; Score 10; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHQKLVFFAQ 10  
Db 22 HHQKLVFFAQ 31

## RESULT 5

US-08-464-247A-3  
; Sequence 3, Application US/08464247A  
; Patent No. 5693478

GENERAL INFORMATION:

APPLICANT: Jacobsen, J. S.

APPLICANT: Vitek, M. P.

TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company

STREET: One Campus Drive

CITY: Parsippany

STATE: New Jersey

COUNTRY: United States

ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,247A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Barnhard, Elizabeth M.

REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 31,844-03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-683-2158

TELEFAX: 201-683-4117

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 63 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-464-247A-3

Query Match 100.0%; Score 10; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHQKLVFFAQ 10  
Db 22 HHQKLVFFAQ 31

## RESULT 6

US-08-464-248A-3  
; Sequence 3, Application US/08464248A  
; Patent No. 5703209

GENERAL INFORMATION:

APPLICANT: Jacobsen, J. S.

APPLICANT: Vitek, M. P.

TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of  
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation  
TITLE OF INVENTION: of B-Amyloid Peptide

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company

STREET: One Cyanamid Plaza

CITY: Wayne

STATE: New Jersey

COUNTRY: United States

ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,248A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Barnhard, Elizabeth M.

REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 31,844-02

TELECOMMUNICATION INFORMATION:

TELEPHONE: (201)831-3246

TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 63 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-464-248A-3

Query Match 100.0%; Score 10; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHQKLVFFAQ 10  
Db 22 HHQKLVFFAQ 31

## RESULT 7

US-08-339-708A-6  
; Sequence 6, Application US/08339708A  
; Patent No. 6037521

GENERAL INFORMATION:

APPLICANT: Sato, Masahiro

APPLICANT: Takashi, Kobayashi

APPLICANT: Tada, No. 6037521hiro

APPLICANT: Shoji, Mikio

APPLICANT: Kavarabayashi, Takeshi

TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S

TITLE OF INVENTION: DISEASE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/339,708A  
FILING DATE: 14-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 306036/93  
FILING DATE: 12-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: SANDERCOCK, COLIN G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 026083/0159  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-339-708A-6

Query Match 100.0%; Score 10; DB 3; Length 99;  
Best Local Similarity 100.0%; Pred. No. 8.6e-05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10  
Db 13 HHQKLVFFAQ 22  
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RESULT 8  
US-08-612-785B-37  
Sequence 37, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Ab peptides that Modulate b-Amyloid  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal  
US-08-612-785B-37

Query Match 90.0%; Score 9; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00024;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9  
Db 3 HHQKLVFFA 11  
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RESULT 9  
US-09-264-709A-2  
Sequence 2, Application US/09264709A  
Patent No. 6320024  
GENERAL INFORMATION:  
APPLICANT: Roberts, Eugene  
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and  
FILE REFERENCE: 2124-310  
CURRENT APPLICATION NUMBER: US/09/264,709A  
CURRENT FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: 08/797,782  
PRIOR FILING DATE: 1997-02-07  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-264-709A-2

Query Match 90.0%; Score 9; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9  
Db 2 HHQKLVFFA 10  
|||||

RESULT 10  
US-08-304-585-7  
Sequence 7, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Maggio, John E.  
APPLICANT: Mantyh, Patrick W.  
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 561415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk



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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-304-585-7

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Query Match 90.0%; Score 9; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.00037; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

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QY 1 HHOKLVFFA 9
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Db 4 HHOKLVFFA 12

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RESULT 11
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-346-849-4
;
; Query Match 90.0%; Score 9; DB 1; Length 28;
; Best Local Similarity 100.0%; Pred. No. 0.0004;
; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 HHOKLVFFA 9
;    |||||
; Db 13 HHOKLVFFA 21
;
; RESULT 12
; US-08-302-808-7
; Sequence 7, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal

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; ORIGINAL SOURCE:  
US-08-302-808-7

Query Match 90.0%; Score 9; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0004;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVEFFA 9  
Db 13 HHQKLVEFFA 21

## RESULT 13

US-08-609-090-2  
; Sequence 2, Application US/08609090  
; Patent No. 5840838  
; GENERAL INFORMATION:  
; APPLICANT: HENSLEY, Kenneth  
; APPLICANT: BUTTERFIELD, D. A.  
; APPLICANT: CARNEY, John M.  
; APPLICANT: AKSENOV, Michael  
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF  
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER  
; STREET: 99 Canal Center Plaza, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/609,090  
; FILING DATE: 29-FEB-1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kraus, Eric J.  
; REGISTRATION NUMBER: 36,190  
; REFERENCE/DOCKET NUMBER: 434-059  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-684-1111  
; TELEFAX: 703-684-1124  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-609-090-2

Query Match 90.0%; Score 9; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0004;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVEFFA 9  
Db 13 HHQKLVEFFA 21

## RESULT 14

US-08-986-948-7  
; Sequence 7, Application US/08986948  
; Patent No. 5955317  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5955317uhiro

; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLIDS OR THEIR  
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/986,948  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/302,808  
; FILING DATE: 15-SEP-1994  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
US-08-986-948-7

Query Match 90.0%; Score 9; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.0004;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVEFFA 9  
Db 13 HHQKLVEFFA 21

## RESULT 15

US-08-293-284A-4  
; Sequence 4, Application US/08293284A  
; Patent No. 5955343  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd  
; APPLICANT: Zhang, Shuguang  
; APPLICANT: Rich, Alexander

```

APPLICANT: DiPersio, C. Michael
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millila Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-284A-4

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Query Match          90.0%; Score 9; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 HHQKLVFFA 9
        |||||
Db      13 HHQKLVFFA 21

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